



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 143545

TO: Vanessa L Ford
Location: REM/3B25/3C18
Art Unit: 1645
Friday, January 28, 2005

Case Serial Number: 10/017168

From: Edward Hart
Location: Biotech-Chem Library
REM-1A55
Phone: 571-272-2512

edward.hart@uspto.gov

Search Notes

Examiner Ford,

Here are the results of the search you requested.

Please feel free to contact me if you have any questions.

Edward Hart

From: Chan, Christina
Sent: Thursday, January 27, 2005 3:16 PM
To: Ford, Vanessa; STIC-Biotech/ChemLib
Subject: RE: In re: 10/017168 sequence search

Please rush. Thanks Chris

Chris Chan

TC 1600 New Hire Training Coordinator and SPE 1644
(571)-272-0841
Remsen, 3E89

-----Original Message-----

From: Ford, Vanessa
Sent: Thursday, January 27, 2005 1:40 PM
To: Chan, Christina
Subject: In re: 10/017168 sequence search

Please search the SEQ ID NOs: 2, 9, 11, 12, 13, 14, 15, 16, 17 and 18. Please include interferences. Please rush.

Vanessa L. Ford
Biotechnology Patent Examiner
Office: REM 3B25
Mailbox: REM 3C18
Phone: 571.272.0857
Art Unit:1645

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STIC

STAFF USE ONLY

Searcher: _____
Searcher Phone: 2- _____
Date Searcher Picked up: 1/28/05
Date Completed: 1/28/05
Searcher Prep/Rev. Time: _____
Online Time: _____

Type of Search

NA Sequence: # 10
AA Sequence: # _____
Structure: # _____
Bibliographic: _____
Litigation: _____
Patent Family: _____
Other: _____

Vendors and cost where applicable

STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: QSP
WWW/Internet: _____
Other(Specify): _____

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OM protein - protein search, using sw model

Run on: January 28, 2005, 11:12:20 ; Search time 379.116 Seconds
(without alignments)
655.635 Million cell updates/sec

Title: US-10-017-168-2
Perfect score: 2188
Sequence: 1 MFVRSDFPKNXTAVEISNLE.....HTKQSHSVSNAPNQRKP 432

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database: 1: uniprot_sprotc:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2188	100.0	432	051953	051953 treponema p
2	2178	99.5	548	093CA4	093CA4 treponema p
3	1478	99.5	428	09ALV6	09ALV6 treponema p
4	1286.5	58.8	393	093CA3	093CA3 treponema p
5	1043.5	47.7	348	09ALV7	09ALV7 treponema p
6	967	44.2	256	083448	083448 treponema p
7	478.5	21.9	227	083449	083449 treponema p
8	368.5	16.8	458	073NG7	073NG7 treponema d
9	285	13.0	1108	09NDIO	09NDIO treponema d
10	285	13.0	1108	09NDIO	09NDIO treponema d
11	279	12.8	5458	09U459	09U459 plasmodium
12	268	12.2	2768	09VC00	09VC00 drosophila
13	267.5	12.2	432	0964C9	0964C9 encephalito
14	267.5	12.2	721	YCF2_OENPI	YCF2_OENPI
15	264.5	12.1	843	06GLM0	06GLM0 xenopus lae
16	264.5	12.1	897	013098	013098 xenopus lae
17	260	11.9	913	013099	013099 xenopus lae
18	260	11.9	913	06DDC0	06DDC0 xenopus lae
19	260	11.9	1110	091255	091255 petromyzon
20	256	11.7	466	06NE60	06NE60 magnetospir
21	256	11.7	466	06NE60	06NE60 magnetospir
22	255.5	11.7	474	0942K8	0942K8 oryza sativ
23	255.5	11.7	567	09HD28	09HD28 homo sapien
24	254.5	11.6	248	09LRH2	09LRH2 leishanus ba
25	252.5	11.5	1167	07SH94	07SH94 neurospora
26	251.5	11.5	1394	08MKE9	08MKE9 bos taurus
27	249.5	11.4	3455	06R5A9	06R5A9 canis fami
28	248.5	11.4	3455	06R5A9	06R5A9 canis fami
29	248.5	11.4	3455	06R5A9	06R5A9 canis fami
30	248	11.3	1070	08LYT0	08LYT0 bacillus an
31	248	11.3	1070	08LYT0	08LYT0 bacillus an
31	248	11.3	1070	AAT29649	AAT29649 bacillus

32	246	11.2	722	026893	026893 trypanosoma
33	246	11.2	982	073CU8	073CU8 bacillus ce
34	246	11.2	982	AAS39897	AAS39897 bacillus
35	245.5	11.2	680	06PCS2	06PCS2 brachydanio
36	245.5	11.2	680	AAS59189	AAS59189 brachydan
37	243	11.1	391	026892	026892 trypanosoma
38	242.5	11.1	1271	025860	025860 plasmodium
39	242	11.1	716	025860	025860 plasmodium
40	239.5	10.9	501	080BK7	080BK7 xenopus lae
41	239	10.9	1554	07RMX1	07RMX1 plasmodium
42	239	10.9	5507	081HN3	081HN3 plasmodium
43	238.5	10.9	501	080AG4	080AG4 salmoxirine
44	237.5	10.9	791	09DGL1	09DGL1 fugu rubrip
45	236.5	10.8	410	096214	096214 encephalito

ALIGNMENTS

RESULT 1
051953 PRELIMINARY; PRT; 432 AA.
ID 051953
AC 051953;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Acidic repeat protein.
OS Treponema pallidum.
OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema.
OX NCBI_TaxID=160;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Nichols;
RA Steiner B.M., Liu H., Rodas B.;
RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF015824; AAB94541.1; -
SQ SEQUENCE 432 AA; 46364 MW; 8FE1E4C5CE46A23 CRC64;

Query Match 100.0%; Score 2188; DB 2; Length 432;
Best Local Similarity 100.0%; Pred. No. 4, 2e-104;
Matches 432; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MFVRSDFPKNXTAVEISNLEKNAQAQAVVIGHAGIFGLVSLAPAAQAQIGVYQAVRV	60
DB	1	MFVRSDFPKNXTAVEISNLEKNAQAQAVVIGHAGIFGLVSLAPAAQAQIGVYQAVRV	60
QY	61	RVVTLGTVRGSGTSDGSLASLPSRVPARPQRPPLSPGHTVPEYRDTVIFDDPR	120
DB	61	RVVTLGTVRGSGTSDGSLASLPSRVPARPQRPPLSPGHTVPEYRDTVIFDDPR	120
QY	121	LVSPLEREVEDAKVVEPASERGGERVEDAKVVEPASERGGERVEDAKVVEPASE	180
DB	121	LVSPLEREVEDAKVVEPASERGGERVEDAKVVEPASERGGERVEDAKVVEPASE	180
QY	181	EREGGERVEDAKVVEPASERGGERVEDAKVVEPASERGGERVEDAKVVEPASE	240
DB	181	EREGGERVEDAKVVEPASERGGERVEDAKVVEPASERGGERVEDAKVVEPASE	240
QY	241	EREGGERVEDAKVVEPASERGGERVEDAKVVEPASERGGERVEDAKVVEPASE	300
DB	241	EREGGERVEDAKVVEPASERGGERVEDAKVVEPASERGGERVEDAKVVEPASE	300
QY	301	EREGGERVEDAKVVEPASERGGERVEDAKVVEPASERGGERVEDAKVVEPASE	360
DB	301	EREGGERVEDAKVVEPASERGGERVEDAKVVEPASERGGERVEDAKVVEPASE	360
QY	361	EREGGERVEDAKVVEPASERGGERVEDAKVVEPASERGGERVEDAKVVEPASE	420
DB	361	EREGGERVEDAKVVEPASERGGERVEDAKVVEPASERGGERVEDAKVVEPASE	420
QY	421	VNSAPNQRKP 432	
DB	421	VNSAPNQRKP 432	
QY	421	VNSAPNQRKP 432	
DB	421	VNSAPNQRKP 432	

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OM protein - protein search, using sw model

Run on: January 28, 2005, 11:05:24 ; Search time 67.3068 Seconds

(without alignments)
617.555 Million cell updates/sec

Title: US-10-017-168-2

Perfect score: 2188

Sequence: 1 MFVRSDFPKNTAVESINLE.....HTKQPSHSVSNAPNQRKP 432

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	967	44.2	256	F71326	hypothetical prote
2	478.5	21.9	227	G71326	hypothetical prote
3	267.5	12.2	721	S29795	hypothetical prote
4	260	11.9	913	T52485	hypothetical prote
5	260	11.9	1110	I51116	hypothetical prote
6	249	11.4	590	A40437	glutamic acid-rich
7	243	11.1	391	S27850	surface antigen TC
8	242.5	11.1	1271	A45555	glutamate rich pro
9	228	10.3	1094	S49313	protein kinase - B
10	225.5	10.3	630	S29796	hypothetical prote
11	224.5	10.3	2109	E89066	protein H05009.1 l
12	224.5	10.3	2109	T33247	hypothetical prote
13	224	10.2	845	A45669	neurofilament trip
14	220.5	10.1	407	EDBE03	neurofilament trip
15	220.5	10.1	296	A54527	immediate-early pr
16	210.5	9.6	506	S47439	120k antigen - pla
17	210.5	9.6	849	S00030	neurofilament trip
18	210	9.6	644	S55395	neurofilament trip
19	206	9.4	679	S28366	recombination repa
20	206	9.4	1560	T30282	calcium-binding pr
21	204	9.3	7962	I38346	elastic titin - hu
22	203	9.3	1621	A82255	hypothetical prote
23	200.5	9.2	1881	H95076	zinc metalloprotei
24	197.5	9.0	916	A27864	neurofilament trip
25	195.5	8.9	544	I36911	involucrin L - dou
26	195.5	8.9	798	I50479	neurofilament medi
27	195	8.9	699	T01029	hypothetical prote
28	191	8.7	924	S27923	gene Lf3 protein -
29	189	8.6	387	D84885	hypothetical prote

30	189	8.6	1262	2	T22523	hypothetical prote
31	188	8.6	837	2	T02761	cuter arm dynein 1
32	187.5	8.6	450	1	C29413	ubiquinol-cytochro
33	187	8.5	880	2	D89756	protein T23B7.2b (
34	186	8.5	518	2	G84488	lin/spm-like transp
35	185	8.5	1187	2	U00316	hypothetical 125k
36	184.5	8.4	784	2	P00009	neurofilament trip
37	184	8.4	706	2	A45990	junctional sarcopl
38	183	8.4	2722	2	T20532	hypothetical prote
39	183	8.4	2738	2	E88320	protein F07A11.6 (
40	182	8.3	333	2	T10738	hypothetical prote
41	182	8.3	699	2	E84565	hypothetical prote
42	182	8.3	754	2	AC2807	Ompa family protei
43	182	8.3	754	2	B97586	hypothetical prote
44	180	8.2	1020	1	QF0UH	neurofilament trip
45	180	8.2	5170	2	T15348	hypothetical prote

ALIGNMENTS

RESULT 1

F71326 hypothetical protein TP0433 - syphilis spirochete

C/Species: Treponema pallidum subsp. pallidum (syphilis spirochete)

C/Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #ext_change 09-Jul-2004

C/Accession: F71326

R/Faaser, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, R.; reon, U.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Uterback, T.; McI they, L.; Weidman, J.; Smith, H.O.; Venter, J.C.

A/Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.

A/Reference number: A71250; MWID:98332770; PMID:9665876

A/Accession: F71326

A/Status: preliminary; nucleic acid sequence not shown; translation not shown

A/Molecule type: DNA

A/Residues: 1-256 <COL>

A/Cross-references: UNIPROT:O83448; GB:AE001220; GB:AE000520; NID:G3322705; PIDN:AA654

A/Experimental source: strain Nichols

C/Genetics:

A/Gene: TP0433

Query Match	Score	DB 2;	Length	256;
Best Local Similarity	99.0%	Pred. No.	3.8e-45;	
Matches	193;	Conservative	0;	Mismatches 2; Indels 0; Gaps 0;
QY	1	MFVRSDFPKNTAVESINLEKNAKQAVVTGAGIPGLIVSLAPAAAQGLGVQAVRV	60	
DB	57	MFVRSDFPKNTAVESINLEKNAKQAVVTGAGIPGLIVSLAPAAAQGLGVQAVRV	116	
QY	61	RVRTTGTVGSGSOTSDGLSLASLPSPVPAPPAOBSPSPAGHTVPEYRDTVFPDDR	120	
DB	117	RVRTTGTVGSGSOTSDGLSLASLPSPVPAPPAOBSPSPAGHTVPEYRDTVFPDDR	176	
QY	121	LVSPISREVEDAPKVEPASERGGERVEDAPKVEPASERGGERVEDAPKVEPAS	180	
DB	177	LVSPISREVEDAPKVEPASERGGERVEDAPKVEPASERGGERVEDAPKVEPAS	236	
QY	181	EREGERVEDAPKV 195		
DB	237	EREGERVEDAPKV 251		

RESULT 2

G71326 hypothetical protein TP0434 - syphilis spirochete

C/Species: Treponema pallidum subsp. pallidum (syphilis spirochete)

C/Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #ext_change 09-Jul-2004

C/Accession: G71326

R/Faaser, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, R.; reon, U.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Uterback, T.; McI they, L.; Weidman, J.; Smith, H.O.; Venter, J.C.

Science 281, 375-388, 1998

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OM protein - protein search, using sw model

Run on: January 28, 2005, 10:59:24 ; Search time 409.335 Seconds
(without alignment)
378.592 Million cell updates/sec

Title: US-10-017-168-2

Perfect score: 2188
Sequence: 1 MFVSDMPKNTAVEISNLE.....HTKOPSHSVSNAPNQRKP 432

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq. length: 0
Maximum DB seq. length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: A_Geneseq_23sep04:*

- 1: Geneseqp1980s:*
- 2: Geneseqp1990s:*
- 3: Geneseqp2000s:*
- 4: Geneseqp2001s:*
- 5: Geneseqp2002s:*
- 6: Geneseqp2003s:*
- 7: Geneseqp2003bs:*
- 8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2188	100.0	432	4	AA048316
2	1480	67.6	312	4	AA048318
3	1048	47.9	232	4	AA048317
4	268	12.2	2768	4	ABB68397
5	255.5	11.7	567	4	AAE13147
6	254.5	11.6	1000	6	ABJ25647
7	249.5	11.4	522	4	AAE02397
8	245	11.2	1018	2	AA097039
9	245	11.2	1018	4	AA097039
10	245	11.2	1018	4	AA097039
11	245	11.2	1018	8	AA097039
12	244.5	11.2	412	8	AA097039
13	244.5	11.2	902	4	AA097039
14	241	11.0	360	2	AA097039
15	240.5	11.0	783	2	AA097039
16	229	10.5	552	7	AA097039
17	229	10.5	1388	6	ABJ38696
18	225.5	10.3	1388	7	ABJ38696
19	224	10.2	845	6	ABJ38696
20	223.5	10.2	864	4	AA097039
21	216.5	9.9	489	4	AB058655
22	214.5	9.8	382	4	AAE02399
23	213.5	9.8	611	2	AA097039
24	213.5	9.8	611	4	AA097039
25	213.5	9.8	611	7	AA097039

26	206	9.4	553	7	ADM05820	Adm05820 Human pro
27	205.5	9.4	474	8	ADN46475	Adn46475 Thermococ
28	205	9.4	869	7	AD160170	Ad160170 Secreted
29	204	9.3	293	4	AAE02398	AAE02398 Canine re
30	204	9.3	466	5	AAE23036	AAE23036 Human thl
31	204	9.3	679	4	ABBS9691	ABBS9691 Drosophil
32	202	9.2	385	6	ABU20070	ABU20070 Protein e
33	200.5	9.2	565	2	AA061247	AA061247 Streptoco
34	200.5	9.2	565	5	ABP54665	ABP54665 S. pneumo
35	200.5	9.2	565	7	AD045299	AD045299 S. pneumo
36	200.5	9.2	1245	6	ABP56885	ABP56885 Streptyl
37	200.5	9.2	1881	3	AA044506	AA044506 Streptoco
38	200.5	9.2	1881	6	ABU01047	ABU01047 S. pneumo
39	200.5	9.2	1881	8	ADM92119	ADM92119 S. pneumo
40	200.5	9.2	2397	6	ABU43308	ABU43308 Protein e
41	200	9.1	654	4	ABBS3266	ABBS3266 Drosophil
42	200	9.1	688	4	ABBS3269	ABBS3269 Drosophil
43	199	9.1	546	6	ABP56886	ABP56886 Streptyl
44	198	9.0	259	1	AA040376	AA040376 Sequence
45	197.5	9.0	554	2	AA020763	AA020763 Human neu

ALIGNMENTS

RESULT 1	AA048316	standard; protein; 432 AA.
XX	AA048316;	
XX	11-SEP-2003 (revised)	
DT	20-APR-2001 (first entry)	
XX	T. pallidum esp. pallidum (nl) acidic repeat protein (arp).	
XX	Treponema pallidum; acidic repeat protein; arp; immunogenic; syphilis;	
KW	yaws; bejel.	
XX	Treponema pallidum; esp. pallidum.	
OS	WO200077486-A2.	
XX	21-DEC-2000.	
PD	14-JUN-2000; 2000WO-US016425.	
XX	14-JUN-1999; 99US-0138981P.	
FR	(USSH) US DEPT HEALTH & HUMAN SERVICES.	
PA	Liu H, Steiner B, Rhodes B;	
XX	WPI; 2001-080711/09.	
DR	N-PSDB; AAC84647.	
XX	Detecting Treponema pallidum in blood, saliva, etc., by detecting	
PT	formation of a complex between immunogenic peptides of acidic repeat	
PT	protein of the bacterium and an antibody present in the biological	
PT	sample.	
XX	Claim 15; Fig 6; 73pp; English.	
XX	The invention relates to a method of detecting presence of Treponema	
CC	pallidum (Tp), anti-treponemal antibodies (Abs), or both in a biological	
CC	sample that involves contacting an acidic repeat protein (arp), or one or	
CC	more isolated immunogenic TP peptides of arp with an Ab containing	
CC	biological sample and then detecting the formation of a complex between	
CC	immunogenic peptides and Ab. The presence of the complex indicates the	
CC	presence of TP. The method is thus useful for diagnosing syphilis, yaws,	
CC	and bejel diseases. The immunogenic peptides or the Abs raised against	
CC	arp, as part of an immunogenic composition, are useful for inducing a	
CC	protective immune response against syphilis, yaws or bejel caused by TP.	

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OM protein - protein search, using sw model

Run on: January 28, 2005, 11:12:20 ; Search time 17.5517 Seconds
(without alignment)

655.635 Million cell updates/sec

Title: US-10-017-168-9
Perfect score: 101
Sequence: 1 PKVPEPASERGEGEREVEDA 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: UniProt_02: *
1: uniprot_sprot: *
2: uniprot_tramb1: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	101	100.0	256	083448	083448 treponema p
2	101	100.0	432	051953	051953 treponema p
3	101	100.0	548	093CA4	093CA4 treponema p
4	97	96.0	227	083449	083449 treponema p
5	97	96.0	348	09ALV7	09ALV7 treponema p
6	97	96.0	393	093CA3	093CA3 treponema p
7	97	96.0	428	09ALV6	09ALV6 treponema p
8	52	51.5	328	SWI6_SCHPO	P40381 schizosach
9	52	51.5	533	07QI86	07QI86 anopheles g
10	51	50.5	77	07XMT2	07XMT2 oryza sativ
11	50	49.5	166	09FXB0	09FXB0 arabidopsis
12	50	49.5	749	YU20_HUMAN	09Y319 homo sapien
13	49	48.5	699	08IIO9	08IIO9 plasmodium
14	49	48.5	719	02S826	02S826 plasmodium
15	48	47.5	226	08S2R0	08S2R0 oryza sativ
16	48	47.5	482	092YV8	092YV8 rhizobium m
17	48	47.5	491	092YV6	092YV6 rhizobium m
18	48	47.5	723	07XG22	07XG22 oryza sativ
19	48	47.5	723	094I06	094I06 oryza sativ
20	48	47.5	742	06P9B2	06P9B2 homo sapien
21	48	47.5	742	AAH60851	AAH60851 homo sapi
22	48	47.5	776	09JG99	09JG99 porcine ast
23	48	47.5	783	09JH64	09JH64 porcine ast
24	47	46.5	122	09KX44	09KX44 yersinia en
25	47	46.5	165	09YRCA	09YRCA drosophila
26	47	46.5	187	09SIO8	09SIO8 arabidopsis
27	47	46.5	193	094I15	094I15 arabidopsis
28	47	46.5	286	08QORUS	08QORUS chimpanzee
29	47	46.5	357	06ZAB0	06ZAB0 oryza sativ
30	47	46.5	357	BAD03360	BAD03360 oryza sat
31	47	46.5	379	Q8MQ44	Q8MQ44 caenorhabdi

32	47	46.5	411	2	Q8MQ45	Q8MQ45 caenorhabdi
33	47	46.5	463	1	Q9P3C3	Q9P3C3 neurospora
34	47	46.5	471	1	P34377	P34377 caenorhabdi
35	47	46.5	541	1	NRL_RAT	P19527 rattus norv
36	47	46.5	572	2	Q9NVZ8	Q9NVZ8 homo sapien
37	47	46.5	678	2	Q8IIC5	Q8IIC5 drosophila
38	47	46.5	752	2	Q8GX86	Q8GX86 homo sapien
39	47	46.5	944	2	Q8CG11	Q8CG11 mus musculu
40	47	46.5	1174	2	Q6ZQ43	Q6ZQ43 mus musculu
41	47	46.5	1174	2	BAC98029	BAC98029 mus muscu
42	47	46.5	1189	2	Q9NTU0	Q9NTU0 homo sapien
43	47	46.5	1431	2	Q9GT23	Q9GT23 homo sapien
44	47	46.5	1841	2	Q3J958	Q3J958 streptomyce
45	46	45.5	159	1	R1SB_CORGL	Q8NQ53 corynebacte

ALIGNMENTS

RESULT 1

083448 PRELIMINARY; PRT; 256 AA.

AC 083448; PRELIMINARY; PRT; 256 AA.
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Hypothetical protein TP0433.
GN OrdereddictNames=TP0433;
OS Treponema pallidum.
OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema.
OX NCBI_Taxid=160;
RN [1]
RP STRAIN=Nichols.
RC MEDLINE=98332770; PubMed=9655876;
RX Fraser C.M., Norris S.J., Weinstein G.M., White O., Sutton G.G.,
RA Dodson R.J., Gwin M.L., Hickey E.K., Clayton R.A., Ketchum K.A.,
RA Sodergren E., Hardham J.M., McLeod M.P., Salzberg S.L., Peterson J.D.,
RA Khalek H.G., Richardson D.L., Howell J.K., Chidambaram M.,
RA Utterback T.R., McDonald L.A., Artach P., Bowman C., Cotton M.D.,
RA Fujii C., Garland S.A., Hatch B., Horst K., Roberts K.M., Sandusky M.,
RA Weidman J.F., Smith H.O., Venter J.C.;
RT "Complete genome sequence of Treponema pallidum, the syphilis
agent." Science 281:1375-1388 (1998).
RL EMBL: AB001220; AAC65421.1; --
DR EMBL; AB001220; AAC65421.1; --
DR PIR; F71326; F71326.
DR TIGR; TP0433; --
KM Complete proteome; Hypothetical protein.
SQ SEQUENCE 256 AA; 27453 MW; E90329D25A119E76 CRC64;

Query Match 100.0%; Score 101; DB 2; Length 256;
Best Local Similarity 100.0%; Pred. No. 5.9e-07;
Matches 20; Conservative 0; Mismatches 0; Incls 0; Gaps 0;
Db 189 PKVPEPASERGEGEREVEDA 208

RESULT 2

051953 PRELIMINARY; PRT; 432 AA.

AC 051953; PRELIMINARY; PRT; 432 AA.
DT 01-JUN-1998 (TREMBLrel. 06, Created)
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE Acidic repeat protein.
OS Treponema pallidum.
OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema.
OX NCBI_Taxid=160;
RN [1]
RP SEQUENCE FROM N.A.

Complete
Genome

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OM protein - protein search, using sw model

Run on: January 28, 2005, 10:59:24 ; Search time 18.9507 Seconds
(without alignment)
378.592 Million cell updates/sec

Title: US-10-017-168-9

Perfect score: 101
Sequence: 1 PKYVEPASEREGGEGREVEDA 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_235ep04:.*
1: geneseqp19808:.*
2: geneseqp19908:.*
3: geneseqp20008:.*
4: geneseqp20018:.*
5: geneseqp20028:.*
6: geneseqp20038:.*
7: geneseqp20038:.*
8: geneseqp20048:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	101	100.0	20	AAB48321	Aab48321 T. pallid
2	101	100.0	432	AAB48316	Aab48316 T. pallid
3	97	96.0	232	AAB48317	Aab48317 T. pallid
4	97	96.0	312	AAB48318	Aab48318 T. pallid
5	85	84.2	21	AAB48325	Aab48325 T. pallid
6	77	76.2	20	AAB48329	Aab48329 T. pallid
7	77	76.2	20	AAB48328	Aab48328 T. pallid
8	77	76.2	20	AAB48327	Aab48327 T. pallid
9	67	66.3	20	AAB48320	Aab48320 T. pallid
10	62	61.4	26	AAB48326	Aab48326 T. pallid
11	58	57.4	20	AAB48330	Aab48330 T. pallid
12	51	50.5	296	AAB48324	Aab48324 Novel hum
13	50	49.5	133	AAG21773	Aag21773 Arabidops
14	50	49.5	163	ADF83534	Adf83534 Human GRI
15	50	49.5	166	AAG21772	Aag21772 Arabidops
16	50	49.5	166	ADN74723	Adn74723 Thale cre
17	50	49.5	749	AAW78419	Aaw78419 Human pro
18	50	49.5	749	AAW78419	Aaw78419 Human pro
19	50	49.5	749	ADP83530	Adp83530 Human GRI
20	50	49.5	749	ADJ69553	Adj69553 Human hea
21	50	49.5	754	AAW20997	Aaw20997 Human nuc
22	50	49.5	757	AAW79403	Aaw79403 Human pro
23	50	49.5	790	AAW41603	Aaw41603 Human ORF
24	48	47.5	888	ABP73624	Abp73624 Candida a
25	47	46.5	69	AAU41010	Aau41010 Propionib

26	47	46.5	69	6	ABM37529	Abm37529 Propionib
27	47	46.5	79	3	AAG61691	Aag61691 Arabidops
28	47	46.5	95	4	AAO04657	Aao04657 Human pol
29	47	46.5	165	4	ABB65571	Abb65571 Drosophil
30	47	46.5	187	3	AAG16629	Aag16629 Arabidops
31	47	46.5	187	3	AAG50350	Aag50350 Arabidops
32	47	46.5	386	4	ABR83349	AbR83349 Partial s
33	47	46.5	386	4	AAW67331	Aaw67331 Amino aci
34	47	46.5	432	4	AAU16231	Aau16231 Human nov
35	47	46.5	432	6	ABU55300	Abu55300 Human nov
36	47	46.5	509	7	ADI60459	Adi60459 Secreted
37	47	46.5	541	7	ADE57652	Ad57652 Rat Prote
38	47	46.5	542	6	ABM04812	Abm04812 Rat NF-L.
39	47	46.5	572	4	ABR92788	AbR92788 Human pro
40	47	46.5	583	4	AAW25397	Aaw25397 Human ORF
41	47	46.5	719	3	AAW42618	Aaw42618 Human ORF
42	47	46.5	942	4	ABG10600	Abg10600 Novel hum
43	47	46.5	1398	5	ABG97491	Abg97491 Human NOV
44	47	46.5	1400	4	ABR83348	AbR83348 AAP-2 pro
45	47	46.5	1445	6	ABR41365	AbR41365 Human DIT

ALIGNMENTS

RESULT 1
ID AAB48321 standard; peptide; 20 AA.
XX
AC AAB48321;
XX
DT 20-APR-2001 (first entry)
XX
DE T. pallidum acidic repeat protein immunogenic peptide arp 3.
XX
KM Treponema pallidum; acidic repeat protein; arp; immunogenic; syphilis;
XX yaws; bejel.
OS Treponema pallidum.
PN WO200077486-A2.
XX
PD 21-DEC-2000.
XX
PF 14-JUN-2000; 2000WO-US016425.
XX
PR 14-JUN-1999; 99US-0138981P.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Liu H, Steiner B, Rhodes B;
XX
WP1; 2001-080711/09.
XX
PT Detecting Treponema pallidum in blood, saliva, etc., by detecting
PT formation of a complex between immunogenic peptides of acidic repeat
PT protein of the bacterium and an antibody present in the biological
PT sample.
PS Claim 15; Fig 11; 73pp; English.
XX
XX The invention relates to a method of detecting presence of Treponema
XX pallidum (TP), anti-treponemal antibodies (Abs), or both in a biological
XX sample that involves contacting an acidic repeat protein (arp), or one or
XX more isolated immunogenic TP peptides of arp with an Ab containing
XX biological sample and then detecting the formation of a complex between
XX immunogenic peptides and Ab. The presence of the complex indicates the
XX presence of TP. The method is thus useful for diagnosing syphilis, yaws,
XX and bejel diseases. The immunogenic peptides or the Abs raised against
XX arp, as part of an immunogenic composition, are useful for inducing a
XX protective immune response against syphilis, yaws or bejel caused by TP.
XX Sequences AAB48319-AAB48330 represent immunogenic peptides of T. pallidum
XX arp protein

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OM protein - protein search, using sw model

Run on: January 28, 2005, 11:12:20 ; Search time 21.936 Seconds
(without alignments)
655.635 Million cell updates/sec

Title: US-10-017-168-11

Perfect score: 124
Sequence: 1 GHAGIPGLVSLAPAAALQIGIVY 25

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	124	100.0	083448	083448 treponema p
2	124	100.0	09ALV7	09ALV7 treponema p
3	124	100.0	093CA3	093CA3 treponema p
4	124	100.0	09ALV6	09ALV6 treponema p
5	124	100.0	051953	051953 treponema p
6	124	100.0	093CA4	093CA4 treponema p
7	63	50.8	073NG7	073NG7 treponema d
8	63	50.8	AA511704	AA511704 treponema d
9	57.5	46.4	089FH6	089FH6 bradyrhizob
10	56.5	45.6	028096	028096 bos taurus
11	56.5	45.6	028097	028097 bos taurus
12	56.5	45.6	028098	028098 bos taurus
13	56.5	45.6	028098	028098 bos taurus
14	55	44.4	09ASV6	09ASV6 caulobacter
15	55	44.4	07VI25	07VI25 prochloroc
16	55	44.4	07VBF7	07VBF7 prochloroc
17	54	43.5	08W008	08W008 sorghum bic
18	53.5	43.1	YK81	YK81 streptomyces
19	53.5	43.1	09XAN5	09XAN5 streptomyces
20	53	42.7	089LRO	089LRO bradyrhizob
21	53	42.7	RNZ	RNZ synchococ
22	53	42.7	07G5W5	07G5W5 anopheles g
23	52.5	42.3	810	810 mus musculus
24	52.5	42.3	810	810 mus musculus
25	52.5	42.3	860	860 mus musculus
26	52	41.9	028099	028099 bos taurus
27	51	41.1	074F10	074F10 geobacter s
28	51	41.1	266	266 AAR34129 geobacter
29	51	41.1	426	426 AAR34129 geobacter
30	51	41.1	0910U3	0910U3 streptomyces
31	51	41.1	453	453 07NWT7 chromobacte

32	51	41.1	557	2	089FZ3	089FZ3 bradyrhizob
33	51	41.1	580	2	08VQ25	08VQ25 myxococcus
34	50.5	40.7	182	2	08C8W0	08C8W0 mus musculus
35	50.5	40.7	593	2	044099	044099 anaplasma m
36	50.5	40.7	622	2	09APG5	09APG5 anaplasma m
37	50.5	40.7	623	2	09APG6	09APG6 anaplasma m
38	50.5	40.7	623	2	09APG7	09APG7 anaplasma m
39	50.5	40.7	623	2	093M65	093M65 anaplasma m
40	50.5	40.7	624	2	06V0Y4	06V0Y4 anaplasma m
41	50.5	40.7	624	2	AA055853	AA055853 anaplasma m
42	50.5	40.7	651	2	07MTV8	07MTV8 anaplasma m
43	50.5	40.7	652	2	044100	044100 anaplasma m
44	50.5	40.7	680	2	06RVB1	06RVB1 anaplasma m
45	50.5	40.7	680	2	AAR33046	AAR33046 anaplasma m

ALIGNMENTS

RESULT 1	083448	PRELIMINARY;	PRT;	256 AA.
AC	083448	01-NOV-1998 (TREMBLrel. 08, Created)		
DT	01-NOV-1998 (TREMBLrel. 08, Last sequence update)			
DE	01-JUN-2003 (TREMBLrel. 24, Last annotation update)			
GN	Hypothetical protein TP0433.			
OS	OrderedListNames=TP0433;			
OC	Treponema pallidum.			
OX	Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema.			
RN	NCBI_TaxID=160;			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=Nichols;			
RX	MEDLINE=98132770; PubMed=9665876;			
RA	Frazer C.M., Norris S.J., Weinstein G.M., White O., Sutton G.G.,			
RA	Dodson R.J., Gwin M.L., Hickey E.K., Clayton R.A., Ketchum K.A.,			
RA	Sodergren E., Hardham J.M., McLeod M.P., Salzborg S.L., Peterson J.D.,			
RA	Khailak H.G., Richardson D.L., Howell J.K., Chidambaram M.,			
RA	Ullrichback T.R., McDonald L.A., Artach P., Bowman C., Cotton M.D.,			
RA	Fujii C., Garland S.A., Hatch B., Horst K., Roberts K.M., Sandusky M.,			
RA	Weisman J.F., Smith H.O., Venter J.C.,			
RT	"Complete genome sequence of Treponema pallidum, the syphilis			
RT	spirochete."			
RL	Science 281:375-388(1998).			
DR	EMBL; AB001220; AAC65421.1; -			
DR	PIR; F71326; F71326.			
DR	TIGR; TP0433; -			
KW	Complete proteome; Hypothetical protein.			
SEQ	SEQUENCE 256 AA; 27453 MW; E90329D25A119E76 CRC64;			
Query Match	100.0%; Score 124; DB 2; Length 256;			
Best Local Similarity	100.0%; Pred. No. 1,9e-08;			
Matches	25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
QY	1 GHAGIPGLVSLAPAAALQIGIVY 25			
DB	87 GHAGIPGLVSLAPAAALQIGIVY 111			
RESULT 2	09ALV7	PRELIMINARY;	PRT;	348 AA.
AC	09ALV7	01-JUN-2001 (TREMBLrel. 17, Created)		
DT	01-DEC-2001 (TREMBLrel. 19, Last sequence update)			
DE	01-OCT-2002 (TREMBLrel. 22, Last annotation update)			
GN	Acidic repeat protein.			
OS	Treponema pallidum (subsp. pertenue) (Yaws treponeme).			
OC	Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema.			
OX	NCBI_TaxID=168;			
RN	[1]			

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OM protein - protein search, using sw model

Run on: January 28, 2005, 11:05:24 ; Search time 3.89507 Seconds
(without alignments)
617.555 Million cell updates/sec

Title: US-10-017-168-11

Perfect score: 124

Sequence: 1 GHAGIPGLVSLAPAAAQIGIGVY 25

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

1: p1r1:*

2: p1r2:*

3: p1r3:*

4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	124	100.0	256 2 F71326	hypotheoretical prote
2	56.5	45.6	747 1 EABO	elastin precursor
3	55	44.4	272 2 F87351	hypotheoretical prote
4	53.5	43.1	242 2 T34851	hypotheoretical prote
5	53.5	43.1	347 2 T35013	probable membrane
6	53	42.7	770 2 S59623	tropoelastin - she
7	52.5	42.3	860 1 EAMS	elastin precursor
8	50.5	40.7	767 2 A35645	major surface prot
9	50	40.3	668 2 F83287	hypotheoretical prote
10	50	40.3	792 1 EAHU	elastin precursor
11	49.5	39.9	377 2 F95948	probable acyltrans
12	49.5	39.9	434 2 S04534	invasin precursor
13	49	39.5	105 2 C97828	hypotheoretical prote
14	49	39.5	349 2 T44856	molybdenum transpo
15	49	39.5	400 2 H83536	hypotheoretical prote
16	49	39.5	459 2 UC7931	cellobiohydrolase
17	49	39.5	603 2 S34130	serine/chreonine-s
18	49	39.5	1053 2 B70987	probable PPE prote
19	48.5	39.1	320 2 F82763	D-alanine-D-alalan
20	48.5	39.1	542 2 AE3057	phosphoglucomutase
21	48.5	39.1	567 2 A96829	phosphoglucomutase
22	48.5	39.1	567 2 A96829	phosphoglucomutase
23	48	38.7	181 2 F83507	elastin precursor
24	48	38.7	195 2 S32123	glycine-rich prote
25	48	38.7	202 2 B87342	hypotheoretical prote
26	48	38.7	334 2 F86462	AIIG-like protein
27	48	38.7	333 2 T34631	probable integral
28	48	38.7	421 2 A26691	cell cycle regulat
29	48	38.7	522 2 T31310	hypotheoretical prote

30	48	38.7	784 2 A26601	elastin precursor
31	47.5	38.3	441 2 H82642	hypotheoretical prote
32	47	37.9	290 2 B87679	integral membrane
33	47	37.9	296 2 I40328	serum-resistance p
34	47	37.9	387 2 T44873	probable secreted
35	47	37.9	464 2 A81480	PTS system, fructo
36	47	37.9	464 2 AG1119	PTS system, fructo
37	47	37.9	614 2 D87410	old protein [impo
38	47	37.9	619 2 A13336	potassium/proton a
39	46.5	37.5	245 2 T03534	precortin-3 methyl
40	46.5	37.5	355 2 H80245	conserved hypotet
41	46.5	37.5	399 2 A55577	formaldehyde dehyd
42	46.5	37.5	476 2 F83286	probable glycosyla
43	46.5	37.5	511 2 D97965	hypotheoretical prote
44	46.5	37.5	511 2 H95097	sugar ABC transpor
45	46.5	37.5	566 2 AH3487	phosphoglucomutase

ALIGNMENTS

RESULT 1

F71326
hypotheoretical protein TP0433 - syphilis spirochete
C/Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
C/Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 09-Jul-2004

C/Accession: F71326

R/Prater: C.M.; Norris, S.J.; Weinstein, G.M.; White, O.; Sutton, G.G.; Dodson, R.;
rean, J.; Khailak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Uettersack, T.;
they, L.; Weidman, J.; Smith, H.O.; Venter, J.C.
Science 281, 375-388, 1998

A/Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.
A/Reference number: AV1250; MUID:98332770; PMID:9665876

A/Accession: F71326

A/Status: preliminary; nucleic acid sequence not shown; translation not shown

A/Molecule type: DNA

A/Residues: 1-256 <COL>

A/Cross-references: UNIPROT:O83448; GB:AEO01220; GB:AEO00520; NID:g3322705; PIDN:AA

A/Experimental source: strain Nichols

C/Genetics:

A/Gene: TP0433

Query Match 100.0%; Score 124; DB 2; Length 256;
Best Local Similarity 100.0%; Pred. No. 1.6e-09;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHAGIPGLVSLAPAAAQIGIGVY 25

DB 87 GHAGIPGLVSLAPAAAQIGIGVY 111

RESULT 2

EABO
elastin precursor, splice form a - bovine

N/Alternate names: tropoelastin

N/Contains: elastin precursor, splice form b; elastin precursor, splice form c

C/Species: Bos primigenius taurus (cattle)

C/Date: 08-Jun-1989 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004

C/Accession: A11865; A26728; B26728; C26728; A22343; I15886

R/ren, H.; Anderson, N.; Ornstein-Goldstein, N.; Baehit, M.M.; Rosenbloom, J.C.; Ab

Biochemistry 28, 2365-2370, 1989

A/Title: Structure of the bovine elastin gene and SI nuclease analysis of alternat

A/Reference number: A11865; MUID:89274159; PMID:2543440

A/Accession: A11865

A/Molecule type: DNA

A/Residues: 1-27 <YEH>

A/Cross-references: UNIPROT:P04985; UNIPROT:Q28101; GB:J02855; NID:G340504; PIDN:AA

J.Raju, K.; Anwar, R.A.

J. Biol. Chem. 262, 5755-5762, 1987

A/Title: Primary structures of bovine elastin a, b, and c deduced from the sequence

A/Reference number: A92640; MUID:87194772; PMID:3032943

A/Accession: A26728

A/Molecule type: mRNA

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OM protein - protein search, using ew model

Run on: January 28, 2005, 10:59:24 ; Search time 23.6884 Seconds
(without alignments)
378.592 Million cell updates/sec

Title: US-10-017-168-11

Perfect score: 124
Sequence: 1 GHAGIPGLIVSLAPAAAOLGIGIV 25

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_23Sep04:*

- 1: geneeqp1980s:*
- 2: geneeqp1990s:*
- 3: geneeqp2000s:*
- 4: geneeqp2001s:*
- 5: geneeqp2002s:*
- 6: geneeqp2003as:*
- 7: geneeqp2003bs:*
- 8: geneeqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	124	100.0	25	AA848323	Aab48323 T. pallid
2	124	100.0	232	AA848317	Aab48317 T. pallid
3	124	100.0	312	AA848318	Aab48318 T. pallid
4	124	100.0	432	AA848316	Aab48316 T. pallid
5	60	48.4	1257	ABO68544	ABO68544 Pseudomon
6	59.5	48.0	843	ABO68524	ABO68524 Novel pro
7	54.5	44.0	1133	ABO8385	ABO8385 Pseudomon
8	51	41.1	28	AA815028	AA815028 Part of e
9	51	41.1	283	AA812779	AA812779 Arabidops
10	51	41.1	306	AA812778	AA812778 Arabidops
11	51	41.1	340	AA812777	AA812777 Arabidops
12	51	41.1	352	ABO66983	ABO66983 Klebsiell
13	51	41.1	437	ABO74993	ABO74993 Pseudomon
14	50.5	40.7	593	AA808404	AA808404 Amv105 en
15	50.5	40.7	652	AA808403	AA808403 Amv105 en
16	50.5	40.7	767	AA807599	AA807599 Sequence
17	50.5	40.7	767	AA808401	AA808401 Amv105 en
18	50	40.3	147	AA801304	AA801304 Human tro
19	50	40.3	171	AA869137	AA869137 Amino aci
20	50	40.3	183	AA801311	AA801311 Human tro
21	50	40.3	183	AA869138	AA869138 Amino aci
22	50	40.3	200	AA801305	AA801305 Human tro
23	50	40.3	216	AA801310	AA801310 Human tro
24	50	40.3	421	ABO70994	ABO70994 Pseudomon
25	50	40.3	472	AA888422	AA888422 Human mem

26	50	40.3	617	7	ADB64761	ADB64761 Human pro
27	50	40.3	630	7	ABO71076	ABO71076 Pseudomon
28	50	40.3	660	2	AA801303	AA801303 Human tro
29	50	40.3	663	7	ADM03792	ADM03792 Human tro
30	50	40.3	692	7	ADB40134	ADB40134 Human pro
31	50	40.3	698	2	AA801302	AA801302 Human tro
32	50	40.3	698	3	AA869069	AA869069 Amino aci
33	50	40.3	711	7	ADB40132	ADB40132 Human tro
34	50	40.3	712	3	AA808630	AA808630 Human NOV
35	50	40.3	730	2	AA846315	AA846315 Amino aci
36	50	40.3	730	3	AA808631	AA808631 Human eia
37	50	40.3	730	5	AA8017360	AA8017360 Fusion pr
38	50	40.3	730	8	ADQ19747	ADQ19747 Human eia
39	50	40.3	731	3	AA869068	AA869068 Human eia
40	50	40.3	731	4	AA866657	AA866657 Amino aci
41	50	40.3	731	6	ABU08725	ABU08725 Human eia
42	50	40.3	731	7	ADL96420	ADL96420 Human eia
43	50	40.3	733	2	AA856653	AA856653 Synthetic
44	50	40.3	733	2	AA801301	AA801301 Amino aci
45	50	40.3	757	7	ABG75223	ABG75223 Human tro

ALIGNMENTS

RESULT 1
AAB48323
ID AAB48323 standard; peptide; 25 AA.

AC AAB48323;
DT 20-APR-2001 (first entry)
DE T. pallidum acidic repeat protein immunogenic peptide arp 5.
XX Treponema pallidum; acidic repeat protein; arp; immunogenic; syphilis;
XX yaws; bejel.
KM Treponema pallidum.
XX Treponema pallidum.
OS Treponema pallidum.
XX Treponema pallidum.
PN WO20007746-A2.
XX WO20007746-A2.
PD 21-DEC-2000.
XX 14-JUN-2000; 2000WO-US016425.
PF 14-JUN-1999; 99US-0138981P.
XX 14-JUN-1999; 99US-0138981P.
PR (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX Liu H, Steiner B, Rhodes B;
XX WPI, 2001-080711/09.

Claim 15, Fig 11; 73pp; English.
The invention relates to a method of detecting presence of Treponema pallidum (TP), anti-treponemal antibodies (Abs), or both in a biological sample that involves contacting an acidic repeat protein (arp), or one or more isolated immunogenic TP peptides of arp with an Ab containing immunogenic peptides and Ab. The presence of the complex between the presence of TP. The method is thus useful for diagnosing syphilis, yaws, and bejel diseases. The immunogenic peptides or the Abs raised against arp, as part of an immunogenic composition, are useful for inducing a protective immune response against syphilis, yaws or bejel caused by TP. Sequences AAB48319-AAB8330 represent immunogenic peptides of T. pallidum arp protein

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OM protein - protein search, using sw model

Run on: January 28, 2005, 11:05:24 ; Search time 3.89507 Seconds
(without alignments)
617.555 Million cell updates/sec

Title: US-10-017-168-12

Perfect score: 137
Sequence: 1 VPARPQRDPUSPPAGHTVPEYRD 25

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	137	100.0	256	2 F71326
2	60	43.8	97	2 G70866
3	52	38.0	212	2 C72464
4	52	38.0	622	2 S56214
5	51	37.2	678	2 G75524
6	51	37.2	982	2 S09810
7	51	37.2	1192	2 T17255
8	51	37.2	2140	2 T18543
9	50	36.5	197	2 S57948
10	50	36.5	417	2 T23024
11	50	36.5	827	2 AC2963
12	50	36.5	881	2 B96320
13	50	36.5	1057	2 T04874
14	50	36.5	1102	2 T28666
15	50	36.5	6420	2 T30283
16	49	35.8	173	2 B39141
17	49	35.8	396	2 UH0633
18	49	35.8	718	1 TNBEF6
19	49	35.8	760	2 T06291
20	49	35.8	900	2 B87957
21	49	35.8	948	2 T26417
22	49	35.8	2115	2 S18480
23	49	35.8	2205	1 MNMYRN
24	48	35.0	101	2 D83375
25	48	35.0	132	2 A5491
26	48	35.0	333	2 H87220
27	48	35.0	443	2 A38219
28	48	35.0	499	1 CPBHS
29	48	35.0	510	1 S43516

30	48	35.0	819	2 A53714	protein kinase (EC
31	48	35.0	1171	2 T35548	hypothetical prote
32	48	35.0	1476	2 A41185	alpha-2 macroglobu
33	48	35.0	3942	2 T42730	Baasoon protein -
34	47.5	34.7	176	2 S02210	con-8 protein - Ne
35	47.5	34.7	312	2 B29350	ery polypeptide, r
36	47.5	34.7	336	2 UC4102	hypothetical 36.9k
37	47.5	34.7	405	2 E70545	hypothetical prote
38	47.5	34.7	445	2 C47757	retrovirus-related
39	47.5	34.7	674	2 T23235	hypothetical prote
40	47.5	34.7	725	2 T35114	probable kinase/ph
41	47.5	34.7	1188	2 S49915	extensin-like prot
42	47	34.3	317	2 E75421	conserved hypothet
43	47	34.3	324	2 S12111	ribonucleoprotein,
44	47	34.3	328	2 T01944	hypothetical prote
45	47	34.3	358	2 F70577	probable lipoprote

ALIGNMENTS

RESULT 1

F71326
hypothetical protein TP0433 - syphilis spirochete

C/Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
C/Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 09-Jul-2004

C/Accession: F71326
R/Fraser, C.M.; Norris, S.J.; Weinstein, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gw

rean, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Uterback, T.; Mc
they, L.; Weidman, J.; Smith, H.O.; Venter, J.C.

Science 281, 375-388, 1998
A/Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.

A/Reference number: A71250; MUID:96332770; PMID:9665876
A/Accession: F71326

A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA

A/Residues: 1-256 <COL>
A/Cross-references: UNIPROT:O83448; GB:A0001220; GB:A000520; NID:g3322705; PIDN:AA065

A/Experimental source: strain Nichols
C/Genetics:
A/Gene: TP0433

Query Match	100.0%	Score 137;	DB 2;	Length 256;
Best Local Similarity	100.0%	Pred. No. 5.3e-11;		
Matches 25;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
DB	1	VPARPQRDPUSPPAGHTVPEYRD	25	
	144	VPARPQRDPUSPPAGHTVPEYRD	168	

RESULT 2

G70866
hypothetical protein RV2472 - Mycobacterium tuberculosis (strain H37RV)

C/Species: Mycobacterium tuberculosis
C/Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004

C/Accession: G70866
R/Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon,

Connor, R.; Davies, R.; Devlin, K.; Felwell, T.; Gentile, S.; Hamlin, N.; Holroyd,
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.

Nature 393, 537-544, 1998
A/Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.

A/Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genom
A/Reference number: A70500; MUID:96295987; PMID:9634230

A/Accession: G70866
A/Status: preliminary; nucleic acid sequence not shown; translation not shown

A/Molecule type: DNA
A/Residues: 1-97 <COL>

A/Cross-references: UNIPROT:O53199; GB:A0021246; GB:AL123456; NID:g33261507; PIDN:CAA16
A/Experimental source: strain H37RV

C/Genetics:
A/Gene: RV2472

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OM protein - protein search, using sw model

Run on: January 28, 2005, 10:59:24 ; Search time 23.6884 Seconds
(without alignments)
378.592 Million cell updates/sec

Title: US-10-017-168-12

Perfect score: 137
Sequence: 1 VPAPPAQRDPSPSPAGHTYPEYRD 25

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729239 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

1: Geneseq_23Sep04:*
2: geneseqp1980s:*
3: geneseqp1980s:*
4: geneseqp2000s:*
5: geneseqp2000s:*
6: geneseqp2000s:*
7: geneseqp2000s:*
8: geneseqp2000s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	137	100.0	25	AA848324	Aab48324 T. pallid
2	137	100.0	232	AA848317	Aab48317 T. pallid
3	137	100.0	312	AA848318	Aab48318 T. pallid
4	137	100.0	432	AA848316	Aab48316 T. pallid
5	59.5	43.4	325	ABO77834	Abog77834 Pseudom
6	57.5	42.0	476	ABG03460	Abog03460 Novel hum
7	57.5	42.0	476	ABO00838	Abog00838 Novel hum
8	57.5	41.6	126	AA82113	Aam82113 Polypepti
9	57	41.6	322	AA840075	Aam40075 Human hae
10	57	41.6	362	ABG03440	Abg03440 Novel hum
11	57	41.6	387	ABG27023	Abg27023 Novel hum
12	57	41.6	491	AA82316	Aaw62316 Mouse pro
13	57	41.6	647	AD867649	Ad867649 Ly1484 Bn
14	57	41.6	647	AD867647	Ad867647 Human Ly4
15	57	41.6	989	ABU21195	Abu21195 Protein e
16	57	41.6	1270	ABU19769	Abu19769 Human MP2
17	57	41.6	1270	AD867643	Ad867643 Human Ly4
18	57	41.6	1270	AD867648	Ad867648 Ly1484 Jo
19	57	41.6	1338	AD840104	Ad840104 Human NOV
20	56	40.9	147	AA002546	Aao02546 Human pol
21	56	40.9	444	AAU52218	Aau52218 Propionib
22	56	40.9	444	ABM48737	Abm48737 Propionib
23	55.5	40.5	614	ABO71464	Abog71464 Pseudom
24	55.5	40.5	2768	AB868397	Ab868397 Drosophil
25	55	40.1	455	AA843987	Aab43987 Human can

26	54	39.4	43	ABG27642	Abg27642 Novel hum
27	54	39.4	104	ADB74290	Adb74290 Mycobacte
28	54	39.4	232	AA509923	Aay50923 Human fet
29	54	39.4	771	ABG29770	Abg29770 Novel hum
30	54	39.4	771	ABG08952	Abg08952 Novel hum
31	53	38.7	95	AAU66811	Aau66811 Novel hum
32	53	38.7	95	AD860145	Ad860145 Connectiv
33	53	38.7	356	ABO71186	Abog71186 Pseudom
34	53	38.7	383	ABO78341	Abog78341 Pseudom
35	53	38.7	654	ABU19399	Abu19399 Human int
36	52.5	38.3	157	ABO72101	Abog72101 Pseudom
37	52.5	38.3	469	ABO83858	Abog83858 Pseudom
38	52.5	38.3	1169	ABG14729	Abg14729 Novel hum
39	52.5	38.3	1294	AA840906	Aam40906 Human pol
40	52	38.0	306	AAU62236	Aau62236 Propionib
41	52	38.0	306	ABM58755	Abm58755 Propionib
42	52	38.0	312	AD822417	Ad822417 Cyanophag
43	52	38.0	622	ABR53818	Abri53818 Protein s
44	52	38.0	622	ADK65006	Adk65006 Disease t
45	52	38.0	625	AD145445	Ad145445 Rice isop

ALIGNMENTS

RESULT 1
ID AAB48324 standard; peptide; 25 AA.
XX
AC AAB48324;
XX
DT 20-APR-2001 (first entry)
XX
DE T. pallidum acidic repeat protein immunogenic peptide arp 6.
XX
KW Treponema pallidum; acidic repeat protein; arp; immunogenic; syphilis;
KW yaws; bejel.
XX
OS Treponema pallidum.
XX
PN WO200077486-A2.
XX
PD 21-DEC-2000.
XX
PF 14-JUN-2000; 2000WO-US016425.
XX
PR 14-JUN-1999; 99US-0138981P.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Liu H, Steiner B, Rhodes B;
XX
DR WPI; 2001-080711/09.
XX
PT Detecting Treponema pallidum in blood, saliva, etc., by detecting
PT formation of a complex between immunogenic peptides of acidic repeat
PT protein of the bacterium and an antibody present in the biological
XX sample.
PS Claim 15; Fig 11; 73pp, English.
XX
XX The invention relates to a method of detecting presence of Treponema
XX pallidum (TP), anti-treponemal antibodies (Abs), or both in a biological
XX sample that involves contacting an acidic repeat protein (arp), or one or
XX more isolated immunogenic TP peptides of arp with an Ab containing
XX immunogenic peptides and then detecting the formation of a complex between
XX presence of TP. The method is thus useful for diagnosing syphilis, yaws,
XX and bejel diseases. The immunogenic peptides or the Abs raised against
XX arp, as part of an immunogenic composition, are useful for inducing a
XX protective immune response against syphilis, yaws or bejel caused by TP.
XX Sequences AAB8319-AA84830 represent immunogenic peptides of T. pallidum
XX arp protein

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OM protein - protein search, using sw model

Run on: January 28, 2005, 11:12:20 ; Search time 18.4293 Seconds
(without alignments)
655.635 Million cell updates/sec

Title: US-10-017-168-13

Perfect score: 105
Sequence: 1 VVEPASERGEGERVEDVPKV 21

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	105	100.0	256 2	083448 Treponema p
2	105	100.0	348 2	09ALV7 Treponema p
3	105	100.0	393 2	093CA3 Treponema p
4	105	100.0	428 2	09ALV6 Treponema p
5	105	100.0	432 2	051953 Treponema p
6	105	100.0	548 2	093CA4 Treponema p
7	98	93.3	227 2	083449 Treponema p
8	56	53.3	533 2	070186 Treponema p
9	55	52.4	3038 1	TRIO HUMAN
10	53	50.5	449 2	09LS16 Treponema p
11	52	49.5	543 2	094A34 Treponema p
12	52	49.5	558 2	095Y17 Treponema p
13	51	48.6	362 2	06UE13 Treponema p
14	51	48.6	362 2	AAT12523 Treponema p
15	51	48.6	1372 2	09VNA6 Treponema p
16	51	48.6	1372 2	085X99 Treponema p
17	50	47.6	183 2	06N585 Treponema p
18	50	47.6	183 2	CAE28537 Treponema p
19	50	47.6	474 2	097Y15 Treponema p
20	50	47.6	585 2	09F3N0 Treponema p
21	50	47.6	699 2	081109 Treponema p
22	50	47.6	719 2	025826 Treponema p
23	49	46.7	471 2	081ZP7 Treponema p
24	49	46.7	1335 2	07MYB2 Treponema p
25	48.5	46.2	328 1	SW16-SCHPO Treponema p
26	48	45.7	154 2	039814 Treponema p
27	48	45.7	226 2	0852R0 Treponema p
28	48	45.7	650 2	06DDE9 Treponema p
29	48	45.7	652 2	08TMI1 Treponema p
30	48	45.7	723 2	07XG22 Treponema p
31	48	45.7	723 2	094106 Treponema p

32	48	45.7	2999 2	08CH17 Treponema p
33	48	45.7	3035 2	08CH18 Treponema p
34	47.5	45.2	379 2	09GL13 Treponema p
35	47	44.8	165 2	09VRC4 Treponema p
36	47	44.8	220 2	08P420 Treponema p
37	47	44.8	221 2	09K959 Treponema p
38	47	44.8	373 2	06H188 Treponema p
39	47	44.8	508 2	045345 Treponema p
40	47	44.8	517 1	GUJA LACRH Treponema p
41	47	44.8	541 1	NFL_RAT Treponema p
42	47	44.8	616 2	08ECM5 Treponema p
43	47	44.8	905 2	09UVAO Treponema p
44	47	44.8	1174 2	06Z043 Treponema p
45	47	44.8	1174 2	BAC98029 Treponema p

ALIGNMENTS

RESULT 1

ID	083448	PRELIMINARY;	PRT;	256 AA.
AC	083448;			
DT	01-NOV-1998	(TREMBLrel. 08, Created)		
DT	01-NOV-1998	(TREMBLrel. 08, Last sequence update)		
DT	01-JUN-2003	(TREMBLrel. 24, Last annotation update)		
DE	Hypothetical protein TP0433.			
CN	OrderedLocustNames=TP0433;			
OS	Treponema pallidum.			
OC	Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema.			
OX	NCBI_TaxID=160;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=Nichols;			
RX	MEDLINE=98332770; PubMed=9665876;			
RA	Frazer C.M., Norris S.J., Weinstein G.M., White O., Sutton G.G.,			
RA	Dodson R.J., Gwin M.L., Hickey E.K., Clayton R.A., Ketchum K.A.,			
RA	Sodergren E., Hardham J.M., McLeod M.P., Salzberg S.L., Peterson J.D.,			
RA	Khairak H.G., Richardson D.L., Howell J.K., Chidambaram M.,			
RA	Kuterback T.R., McDonald L.A., Artlisch P., Bowman C., Cotton M.D.,			
RA	Fuji C., Garland S.A., Hatch B., Horst K., Roberts K.M., Sandusky M.,			
RA	Weidman J.F., Smith H.O., Venter J.C.;			
RT	"Complete genome sequence of Treponema pallidum, the syphilis			
RT	spirochete."			
RL	Science 281:375-388(1998).			
DR	EMBL; AE001220; AAC65421.1; --			
DR	PIR; F71326; F71326.			
KW	Complete proteome; Hypothetical protein.			
KM	SEQUENCE 256 AA; 27453 MW; E90329D25A119E76 CRC64;			
SQ				
	Query Match	100.0%;	Score 105; DB 2;	Length 256;
	Best Local Similarity	100.0%;	Pred. No. 1,3e-07;	
	Matches 21;	Conservative 0;	Mismatches 0;	Indels 0; Gaps 0;
Oy	1 VVEPASERGEGERVEDVPKV 21			
Db	231 VVEPASERGEGERVEDVPKV 251			
	RESULT 2			
ID	09ALV7	PRELIMINARY;	PRT;	348 AA.
AC	09ALV7;			
DT	01-JUN-2001	(TREMBLrel. 17, Created)		
DT	01-DEC-2001	(TREMBLrel. 19, Last sequence update)		
DT	01-OCT-2002	(TREMBLrel. 22, Last annotation update)		
DE	Acidic repeat protein.			
CN	Name=arp;			
OS	Treponema pallidum (subsp. pertenue) (Yaws treponeme).			
OC	Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema.			
OX	NCBI_TaxID=160;			
RN	[1]			

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OM protein - protein search, using sw model

Run on: January 28, 2005, 10:59:24 ; Search time 19.8963 seconds
(without alignments)
378.592 Million cell updates/sec

Title: US-10-017-168-13
Perfect score: 105
Sequence: 1 VVEPASREGEREVEDVPKV 21

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: A_Geneseq_23sep04:
1: geneseqp1980s:
2: geneseqp1990s:
3: geneseqp2000s:
4: geneseqp2001s:
5: geneseqp2002s:
6: geneseqp2003as:
7: geneseqp2003bs:
8: geneseqp2004s:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	105	100.0	21	4	AB48325 T. pallid
2	105	100.0	232	4	AB48317 T. pallid
3	105	100.0	312	4	AB48318 T. pallid
4	105	100.0	432	4	AB48316 T. pallid
5	85	81.0	20	4	AB48321 T. pallid
6	65	61.9	20	4	AB48329 T. pallid
7	65	61.9	20	4	AB48328 T. pallid
8	65	61.9	20	4	AB48327 T. pallid
9	62	59.0	26	4	AB48326 T. pallid
10	55	52.4	20	4	AB48320 T. pallid
11	55	52.4	2980	4	ABG20756 Novel hum
12	55	52.4	3038	4	ABG17025 Novel hum
13	55	52.4	3038	4	ABM32684 Human Tr1
14	55	52.4	3038	6	ABO07226 Human p53
15	55	52.4	3060	4	ABG06311 Novel hum
16	53	50.5	20	4	AB48330 T. pallid
17	53	50.5	449	5	ABR93640 Hetericida
18	51	48.6	1167	4	ABBS7757 Drosophila
19	49	46.7	121	7	ADP60314 Human con
20	49	46.7	216	7	ADP58964 Human pol
21	49	46.7	471	6	AAO26610 Human 6-O
22	49	46.7	472	8	ADH72050 Human pro
23	49	46.7	472	8	ADH72052 Human pro
24	49	46.7	472	8	ADH72038 Human pro
25	49	46.7	944	5	ADH16666 Human NOV

ALIGNMENTS

26	49	46.7	944	8	ADN42320 Human nov
27	48	45.7	154	2	AA228301 Amino aci
28	48	45.7	652	7	ADM26621 Hyperther
29	47.5	45.2	296	4	ABG15624 Novel hum
30	47	44.8	165	4	ABBS5571 Drosophila
31	47	44.8	541	7	ADP57652 Rat Prote
32	47	44.8	542	6	ABM04812 Rat NF-L
33	47	44.8	3353	5	AAU82706 Amino aci
34	46	43.8	33	2	AA872825 Mitocobin r
35	46	43.8	159	4	AB79915 Corynebact
36	46	43.8	159	4	AB79916 Corynebact
37	46	43.8	159	4	AA91507 C glutami
38	46	43.8	163	7	ADF83534 Human GRI
39	46	43.8	187	8	ADM57223 A thalian
40	46	43.8	305	7	ADN95157 Human BEC
41	46	43.8	306	8	ADO24505 Human PRO
42	46	43.8	409	5	AAO17170 Human sec
43	46	43.8	409	5	AAE21624 Human gen
44	46	43.8	409	5	ABG64754 Human alb
45	46	43.8	409	7	ADN95109 Human LEC

RESULT 1
ID AAB48325
AAB48325 standard; peptide: 21 AA.
AC AAB48325;
DT 20-APR-2001 (first entry)
XX T. pallidum acidic repeat protein immunogenic peptide arp 7.
DE Treponema pallidum; acidic repeat protein; arp; immunogenic; syphilis;
KW yaws; bejel.
XX Treponema pallidum.
OS WO200077486-A2.
XX 21-DEC-2000.
XX 14-JUN-2000; 2000WO-US016425.
XX 14-JUN-1999; 99US-0138981P.
XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX Liu H, Steiner B, Rhodes B;
XX WPI; 2001-080711/09.
XX Detecting Treponema pallidum in blood, saliva, etc., by detecting
PT formation of a complex between immunogenic peptides of acidic repeat
PT protein of the bacterium and an antibody present in the biological
PT sample.
XX Claim 15, Fig 11; 73pp, English.
PS The invention relates to a method of detecting presence of Treponema
CC pallidum (TP), anti-treponemal antibodies (Abs), or both in a biological
CC sample that involves contacting an acidic repeat protein (arp), or one or
CC more isolated immunogenic TP peptides of arp with an Ab containing
CC biological sample and then detecting the formation of a complex between
CC immunogenic peptides and Ab. The presence of the complex indicates the
CC presence of TP. The method is thus useful for diagnosing syphilis, yaws,
CC and bejel diseases. The immunogenic peptides or the Abs raised against
CC arp, as part of an immunogenic composition, are useful for inducing a
CC protective immune response against syphilis, yaws or bejel caused by TP.
CC Sequences AAB48319-AAB48330 represent immunogenic peptides of T. pallidum
CC arp protein

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OM protein - protein search, using sw model

Run on: January 28, 2005, 11:05:24 ; Search time 4.05087 Seconds
(without alignments)
617.555 Million cell updates/sec

Title: US-10-017-168-14

Perfect score: 137
Sequence: 1 VVEPAGHGEGEREVASQHTKPSHS 26

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: p1r1:
2: p1r2:
3: p1r3:
4: p1r4:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	137	100.0	227	2	G71326
2	62	45.3	256	2	F71326
3	52	38.0	303	2	B83367
4	52	38.0	556	2	T03114
5	49.5	36.1	2722	2	T20532
6	49.5	36.1	2738	2	E88320
7	49	35.8	551	2	H69371
8	49	35.8	555	2	D71298
9	49	35.8	2649	2	T51023
10	48	35.0	546	1	S71008
11	48	35.0	723	2	AG0887
12	47	34.3	445	2	S73703
13	47	34.3	467	2	F86468
14	47	34.3	1154	2	S69206
15	47	34.3	1236	2	T50904
16	46.5	33.9	161	2	AF0536
17	46.5	33.9	519	2	S54300
18	46.5	33.9	695	2	S62400
19	46	33.6	510	2	G96022
20	46	33.6	510	2	B87494
21	46	33.6	707	2	A48686
22	46	33.6	1034	2	A36108
23	45.5	33.2	277	2	T49533
24	45.5	33.2	813	2	T12506
25	45.5	33.2	1280	2	T00365
26	45	32.8	184	2	AF0298
27	45	32.8	330	2	A82538
28	45	32.8	343	2	A86241
29	45	32.8	385	1	I39498

30	45	32.8	413	2	B65088	hypothetical prote
31	45	32.8	424	2	E86367	protein F26F24.22
32	45	32.8	430	2	C23351	serendipity (ery)
33	45	32.8	525	2	A99953	hypothetical prote
34	45	32.8	689	2	S39531	exonuclease ABC c
35	45	32.8	735	2	S54147	alpha adducin - ra
36	45	32.8	739	2	D91116	hypothetical prote
37	45	32.8	739	2	D85961	hypothetical prote
38	45	32.8	1200	2	T48194	hypothetical prote
39	45	32.8	1785	2	T21558	hypothetical prote
40	45	32.8	1929	2	T21559	hypothetical prote
41	44.5	32.5	384	2	A46403	transcription fact
42	44.5	32.5	625	2	A34615	profilaggrin - rat
43	44.5	32.5	650	2	T46660	nulur controller-
44	44	32.1	134	2	H75316	conserved hypothet
45	44	32.1	328	2	A11940	hypothetical prote

ALIGNMENTS

RESULT 1
G71326
hypothetical protein TP0434 - syphilis spirochete
C/Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
C/Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 09-Jul-2004
C/Accession: G71326
R/Fraser, C.M.; Norris, S.J.; Weinstein, G.M.; White, O.; Sutton, G.G.; Dodson, R.; GwJ
rson, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Uterback, T.; McI
they, L.; Weidman, J.; Smith, H.O.; Venter, J.C.
Science 281, 375-388, 1998
A/Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.
A/Reference number: A71250; PMID:98332770; PMID:9665876
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Accession: G71326
A/Molecule type: DNA
A/Residues: 1-227 <COL>
A/Cross-references: UNIPROT:083449; GB:AE001220; GB:AE000520; NID:G3322705; PIDN:AAC654
A/Experimental source: strain Nichols
C/Genetics:
A/Gene: TP0434

Query Match 100.0%; Score 137; DB 2; Length 227;
Best Local Similarity 100.0%; Pred. No. 8.4e-13;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VVEPAGHGEGEREVASQHTKPSHS 26
Db 74 VVEPAGHGEGEREVASQHTKPSHS 99

RESULT 2
F71326
hypothetical protein TP0433 - syphilis spirochete
C/Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
C/Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 09-Jul-2004
C/Accession: F71326
R/Fraser, C.M.; Norris, S.J.; Weinstein, G.M.; White, O.; Sutton, G.G.; Dodson, R.; GwJ
rson, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Uterback, T.; McI
they, L.; Weidman, J.; Smith, H.O.; Venter, J.C.
Science 281, 375-388, 1998
A/Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.
A/Reference number: A71250; PMID:98332770; PMID:9665876
A/Accession: F71326
A/Molecule type: DNA
A/Residues: 1-256 <COL>
A/Cross-references: UNIPROT:083448; GB:AE001220; GB:AE000520; NID:G3322705; PIDN:AAC654
A/Experimental source: strain Nichols
C/Genetics:
A/Gene: TP0433

Query Match 45.3%; Score 62; DB 2; Length 256;

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OM protein - protein search, using sw model

Run on: January 28, 2005, 10:59:24 ; Search time 24.6359 Seconds
(without alignment)
378.592 Million cell updates/sec

Title: US-10-017-168-14
Perfect score: 137
Sequence: 1 VPEPAGSGEGREVAQHTKQPSHS 26

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: A_Geneseq_23Sep04:*

- 1: Geneseqp1980s:*
- 2: Geneseqp1990s:*
- 3: Geneseqp2000s:*
- 4: Geneseqp2001s:*
- 5: Geneseqp2002s:*
- 6: Geneseqp2003as:*
- 7: Geneseqp2003bs:*
- 8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	137	100.0	26	4	AA848326 T. pallid
2	137	100.0	432	4	AA848316 T. pallid
3	121	88.3	232	4	AA848317 T. pallid
4	121	88.3	312	4	AA848318 T. pallid
5	69	50.4	20	4	AA848330 T. pallid
6	62	45.3	20	4	AA848321 T. pallid
7	62	45.3	21	4	AA848325 T. pallid
8	56	40.9	339	4	AA848329 T. pallid
9	53	38.7	20	4	AA848328 T. pallid
10	53	38.7	20	4	AA848327 T. pallid
11	53	38.7	20	4	AA848326 T. pallid
12	53	38.7	683	7	ADD44867 Rat Prote
13	52	38.0	349	7	ABO77085 Pseudomon
14	52	38.0	478	8	ADJ92061 Soybean h
15	51.5	37.6	330	4	AA894271 Human pro
16	51.5	37.6	330	4	AA894271 Human pro
17	51.5	37.6	330	7	ADJ70056 Human hea
18	51.5	37.6	572	4	AAU32685 Novel hum
19	51	37.2	70	4	AAU14734 Peptide #
20	51	37.2	70	4	AB833699 Peptide #
21	51	37.2	70	4	AA827157 Peptide #
22	51	37.2	70	4	AB828514 Peptide #
23	51	37.2	70	4	AB819148 Protein #
24	51	37.2	70	4	AA866872 Human bon
25	51	37.2	70	4	AA854467 Human bra

26	51	37.2	70	4	AB848537 Human liv
27	51	37.2	70	4	AA802456 Peptide #
28	51	37.2	70	5	AB836529 Human pep
29	51	37.2	440	7	ABO70847 Pseudomon
30	49.5	36.1	541	4	AB868621 Drosophila
31	49.5	36.1	1473	4	AB868024 Drosophila
32	49	35.8	105	8	ADP83532 Breast ep
33	49	35.8	120	8	ADP83529 Breast ep
34	49	35.8	125	4	AB813074 Novel hum
35	49	35.8	125	4	AB813076 Novel hum
36	49	35.8	125	7	AD809109 Novel pro
37	49	35.8	128	5	ABP42456 Human ova
38	49	35.8	155	8	ADP83527 Breast ep
39	49	35.8	157	8	ADP83530 Breast ep
40	49	35.8	294	7	ABO73357 Pseudomon
41	49	35.8	478	5	AAU96770 Lycopersi
42	49	35.8	539	7	ABO73745 Pseudomon
43	48.5	35.4	109	4	AB815090 Human ner
44	48.5	35.4	330	4	AAU45385 Propionib
45	48.5	35.4	330	6	ABM41904 Propionib

ALIGNMENTS

RESULT 1	
AA848326	AB848326 standard; peptide; 26 AA.
ID	AA848326
XX	AA848326:
AC	
XX	
DT	20-APR-2001 (first entry)
XX	
DE	T. pallidum acidic repeat protein immunogenic peptide arp 8.
XX	
KW	Treponema pallidum; acidic repeat protein; arp; immunogenic; syphilis;
KW	yaws; bejel.
XX	
OS	Treponema pallidum.
XX	
PN	W0200077486-A2.
XX	
PD	21-DEC-2000.
XX	
PF	14-JUN-2000; 2000WO-US016425.
XX	
RR	14-JUN-1999; 99US-0138981P.
XX	
PA	(USSH) US DEPT HEALTH & HUMAN SERVICES.
XX	
PI	Liu H, Steiner B, Rhodes B;
XX	
DR	WPI; 2001-080711/09.
XX	
PT	Detecting Treponema pallidum in blood, saliva, etc., by detecting
PT	formation of a complex between immunogenic peptides of acidic repeat
PT	protein of the bacterium and an antibody present in the biological
PT	sample.
XX	
PS	Claim 15; Fig 11; 73pp; English.
XX	
CC	The invention relates to a method of detecting presence of Treponema
CC	pallidum (TP), anti-treponemal antibodies (Abs), or both in a biological
CC	sample that involves contacting an acidic repeat protein (arp), or one or
CC	more isolated immunogenic TP peptides of arp with an Ab containing
CC	biological sample and then detecting the formation of a complex between
CC	immunogenic peptides and Ab. The presence of the complex indicates the
CC	presence of TP. The method is thus useful for diagnosing syphilis, yaws,
CC	and bejel diseases. The immunogenic peptides or the Abs raised against
CC	arp, as part of an immunogenic composition, are useful for inducing a
CC	protective immune response against syphilis, yaws or bejel caused by TP.
CC	Sequences AA848319-AA848330 represent immunogenic peptides of T. pallidum
CC	arp protein

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OM protein - protein search, using sw model

Run on: January 28, 2005, 10:59:24 ; Search time 18.9507 Seconds
(without alignments)
378.592 Million cell updates/sec

Title: US-10-017-168-15

Perfect score: 101
Sequence: 1 EVEDVPKVEPASEEGGER 20

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: A_Geneseq_23sep04:*

- 1: Geneseqp1980s:*
- 2: Geneseqp1990s:*
- 3: Geneseqp2000s:*
- 4: Geneseqp2001s:*
- 5: Geneseqp2002s:*
- 6: Geneseqp2003as:*
- 7: Geneseqp2003bs:*
- 8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	101	100.0	20	AA048327	Aab48327 T. pallid
2	101	100.0	232	AA048317	Aab48317 T. pallid
3	101	100.0	312	AA048318	Aab48318 T. pallid
4	101	100.0	432	AA048316	Aab48316 T. pallid
5	97	96.0	20	AA048329	Aab48329 T. pallid
6	96	95.0	20	AA048328	Aab48328 T. pallid
7	87	86.1	20	AA048320	Aab48320 T. pallid
8	82	81.2	20	AA048330	Aab48330 T. pallid
9	77	76.2	20	AA048321	Aab48321 T. pallid
10	65	64.4	21	AA048325	Aab48325 T. pallid
11	60	59.4	19	AA048319	Aab48319 T. pallid
12	53	52.5	26	AA048326	Aab48326 T. pallid
13	50	49.5	79	AA061691	Aag61691 Arabidops
14	50	49.5	187	AA016629	Aag16629 Arabidops
15	50	49.5	187	AA050350	Aag50350 Arabidops
16	49	48.5	170	AA055215	Aag55215 Human pro
17	49	48.5	266	AA080279	Aab80279 Human pro
18	49	48.5	266	AA064379	Aab64379 Amino aci
19	49	48.5	266	AA039738	Aab39738 Human pol
20	49	48.5	277	AA080305	Aab80305 Human pro
21	49	48.5	277	AA080347	Aab80347 Human pro
22	49	48.5	288	AA080343	Aab80343 Human pro
23	49	48.5	289	AA041524	Aab41524 Human pol
24	49	48.5	304	AA057037	Aab57037 Human pro
25	49	48.5	519	AA020235	Aab20235 Protein e

26	48	47.5	296	4	AB015624	fbg15624 Novel hum
27	48	47.5	547	6	AB015867	fbm15867 Mycobacte
28	48	47.5	754	7	AD036201	ade36201 Klebsiell
29	48	47.5	754	7	AD036160	ade36160 Klebsiell
30	47.5	47.0	792	4	AA082199	aa082199 S. epider
31	47.5	47.0	801	5	AB040739	abp40739 Staphyloc
32	47	46.5	117	6	ADA15777	ada15777 Human GAG
33	47	46.5	117	6	AD085417	ad085417 Human GAG
34	47	46.5	510	8	AD008680	ad008680 Clona int
35	47	46.5	1022	4	AB020687	ab020687 Novel hum
36	47	46.5	1278	6	AB074682	ab074682 Human CGD
37	47	46.5	2091	8	AD061449	ad061449 Human KXP
38	47	46.5	2193	6	AB042219	abr42219 Human pro
39	47	46.5	2219	8	AD000364	adn00364 Novel hum
40	47	46.5	2245	8	AD096651	ad096651 Human Nim
41	46.5	46.0	571	7	AB077402	abo77402 Pseudomon
42	46	45.5	60	5	AB034774	abp34774 Human ORF
43	46	45.5	171	3	AA080178	aa080178 Arabidops
44	46	45.5	197	3	AA080177	aa080177 Arabidops
45	46	45.5	226	3	AA080176	aa080176 Arabidops

ALIGNMENTS

RESULT 1
AA048327
ID AA048327 standard; peptide; 20 AA.

XX AA048327:

AC 20-APR-2001 (first entry)

DE T. pallidum acidic repeat protein immunogenic peptide arp 9.

XX Treponema pallidum; acidic repeat protein; arp; immunogenic; syphilis;

KM yaws; bejel.

XX Treponema pallidum.

OS WO200077486-A2.

PN 21-DEC-2000.

XX 14-JUN-2000; 2000MO-US016425.

PF 14-JUN-1999; 99US-0138981P.

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

FA Liu H. Steiner B, Rhodes B;

XX WPI; 2001-080711/09.

DR Detecting Treponema pallidum in blood, saliva, etc., by detecting

FT formation of a complex between immunogenic peptides of acidic repeat

PT protein of the bacterium and an antibody present in the biological

XX sample.

XX Claim 15; Fig 11; 73pp; English.

PS The invention relates to a method of detecting presence of Treponema

XX pallidum (Tp), anti-treponemal antibodies (Abs), or both in a biological

CC sample that involves contacting an acidic repeat protein (arp), or one or

CC more isolated immunogenic TP peptides of arp with an Ab containing

CC biological sample and then detecting the formation of a complex between

CC immunogenic peptides and Ab. The presence of the complex indicates the

CC presence of TP. The method is thus useful for diagnosing syphilis, yaws,

CC and bejel diseases. The immunogenic peptides or the Abs raised against

CC arp, as part of an immunogenic composition, are useful for inducing a

CC protective immune response against syphilis, yaws or bejel caused by TP.

CC Sequences AA048319-AA048330 represent immunogenic peptides of T. pallidum

CC arp protein

Jan 28 13:02:54 2005

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OM protein - protein search, using sw model

Run on: January 28, 2005, 11:05:24, Search time 3.11606 Seconds

(Without alignments)
617.555 Million cell updates/sec

Title: US-10-017-168-15

Perfect score: 101
Sequence: 1 EVEDPKVPEASEREGGER 20

Scoring table: ELOSUM62
Gapop 10.0, Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: PIR 79:*

1: PIR1: *
2: PIR2: *
3: PIR3: *
4: PIR4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	97	96.0	256	2 F71326	hypothetical prote
2	82	81.2	227	2 G71326	hypothetical prote
3	51.5	51.0	153	1 B69215	conserved hypotet
4	50	49.5	184	2 D84603	hypothetical prote
5	48	47.5	547	2 E70650	phosphoglucosylase
6	47	46.5	308	2 T17946	hypothetical prote
7	47	46.5	1151	2 T24541	hypothetical prote
8	46.5	46.0	946	2 D96503	protein F9C16.9 (I
9	46	45.5	437	2 C35147	integrase homolog
10	45	44.6	99	2 A55819	nonhistone chromos
11	45	44.6	178	2 E95994	hypothetical prote
12	45	44.6	264	1 G69884	conserved hypotet
13	45	44.6	798	2 T31022	hypothetical prote
14	45	44.6	873	2 T16282	hypothetical prote
15	45	44.6	1350	2 G36793	hypothetical prote
16	44	43.6	220	2 S26685	hypothetical prote
17	44	43.6	251	1 C36044	CAMP response elem
18	44	43.6	306	2 T00177	indole-3-glycerol
19	44	43.6	306	2 G89988	hypothetical prote
20	44	43.6	344	2 JCS601	hypothetical prote
21	44	43.6	681	2 E81815	CAMP response elem
22	44	43.6	882	1 S22700	probable transpos
23	44	43.6	897	2 E68202	amphiphysin chic
24	44	43.6	1069	2 T00043	valine-tRNA ligase
25	44	43.6	1072	2 T00041	BH-protocadherin a
26	44	43.6	1200	2 T00042	BH-protocadherin p
27	44	43.6	1537	2 JC4172	DNA (cytosine-5-)-
28	44	43.6	1537	2 JC4172	hypothetical prote
29	43	42.6	133	2 T36525	hypothetical prote

30	43	42.6	199	2 AB2847	conserved hypotet
31	43	42.6	210	2 C87305	hypothetical prote
32	43	42.6	217	2 C37944	CAMP response elem
33	43	42.6	220	2 A75287	response regulator
34	43	42.6	227	2 B97624	hypothetical prote
35	43	42.6	229	2 B37944	CAMP response elem
36	43	42.6	229	2 A37944	CAMP response elem
37	43	42.6	341	2 S36101	CAMP response elem
38	43	42.6	341	2 S20827	CAMP response elem
39	43	42.6	341	2 S2686	CAMP response elem
40	43	42.6	356	2 B71023	CAMP response elem
41	43	42.6	369	2 A39157	hypothetical prote
42	43	42.6	434	2 T47545	probable RNA helic
43	43	42.6	542	2 E84250	nonodehydroascorba
44	43	42.6	668	1 COBEM1	acetyl-CoA synthet
45	43	42.6	670	1 YCMT	Uls2 protein - hum
					acetolactate synth

ALIGNMENTS

RESULT 1

F71326 hypothetical protein TP0433 - syphilis spirochete

C:Species: Treponema pallidum subsp. pallidum (syphilis spirochete)

C>Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 09-Jul-2004

C:Accession: F71326

R:Fraser, C.M.; Norris, S.J.; Weinstein, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwison, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Uettermann, T.; McDermott, L.; Weidman, J.; Smith, H.O.; Venter, J.C.

A:Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.

A:Reference number: A71250; MUID:98332770; PMID:965876

A:Accession: F71326

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-256 <COL>

A:Cross-references: UNIPROT:O83448; GB:AE001220; GB:AE000520; NID:G3322705; PIDN:AAC654

A:Experimental source: strain Nichols

C:Genetics:

A:Gene: TP0433

Query Match 96.0%; Score 97; DB 2; Length 256;

Best Local Similarity 95.0%; Pred. No. 3.8e-07;

Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EVEDPKVPEASEREGGER 20

DB 184 EVEDPKVPEASEREGGER 203

RESULT 2

G71326 hypothetical protein TP0434 - syphilis spirochete

C:Species: Treponema pallidum subsp. pallidum (syphilis spirochete)

C>Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 09-Jul-2004

C:Accession: G71326

R:Fraser, C.M.; Norris, S.J.; Weinstein, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwison, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Uettermann, T.; McDermott, L.; Weidman, J.; Smith, H.O.; Venter, J.C.

A:Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.

A:Reference number: A71250; MUID:98332770; PMID:965876

A:Accession: G71326

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-227 <COL>

A:Cross-references: UNIPROT:O83449; GB:AE001220; GB:AE000520; NID:G3322705; PIDN:AAC654;

A:Experimental source: strain Nichols

C:Genetics:

A:Gene: TP0434

Query Match 81.2%; Score 82; DB 2; Length 227;

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OM protein - protein search, using sw model

Run on: January 28, 2005, 11:12:20 ; Search time 17.5517 seconds.
(without alignments)

655,635 Million cell updates/sec

Title: US-10-017-168-15

Perfect score: 101
Sequence: 1 EVEDVPKVVPEPASEREGGER 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : UniProt_02:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	101	100.0	348	2	Q9ALV7
2	101	100.0	393	2	Q93CA3
3	101	100.0	428	2	Q9ALV6
4	101	100.0	432	2	Q93CA4
5	101	100.0	548	2	Q93CA4
6	97	96.0	256	2	Q93CA4
7	82	81.2	227	2	Q93CA4
8	51.5	51.0	153	1	Y862_METTH
9	50	49.5	187	2	Q93CA3
10	50	49.5	193	2	Q93CA3
11	50	49.5	238	2	Q93CA3
12	50	49.5	238	2	Q93CA3
13	50	49.5	1174	2	Q93CA3
14	48	47.5	256	2	Q93CA3
15	48	47.5	482	2	Q93CA3
16	48	47.5	482	2	Q93CA3
17	48	47.5	547	2	Q93CA3
18	48	47.5	547	2	Q93CA3
19	48	47.5	2192	2	Q93CA3
20	47.5	47.0	792	2	Q93CA3
21	47	46.5	178	2	Q93CA3
22	47	46.5	178	2	Q93CA3
23	47	46.5	266	2	Q93CA3
24	47	46.5	280	2	Q93CA3
25	47	46.5	280	2	Q93CA3
26	47	46.5	308	2	Q93CA3
27	47	46.5	357	2	Q93CA3
28	47	46.5	357	2	Q93CA3
29	47	46.5	1159	2	Q93CA3
30	47	46.5	1165	2	Q93CA3
31	47	46.5	1165	2	Q93CA3

32	47	46.5	2297	1	WNK2_HUMAN
33	46.5	46.0	946	2	Q91P09
34	46	45.5	174	2	Q93CA3
35	46	45.5	200	2	Q93CA3
36	46	45.5	200	2	Q93CA3
37	46	45.5	290	2	Q93CA3
38	46	45.5	290	2	Q93CA3
39	46	45.5	348	2	Q93CA3
40	46	45.5	371	2	Q93CA3
41	46	45.5	383	2	Q93CA3
42	46	45.5	434	2	Q93CA3
43	46	45.5	434	2	Q93CA3
44	46	45.5	434	2	Q93CA3
45	46	45.5	437	1	INTR_SACER

ALIGNMENTS

RESULT 1

Q9ALV7 PRELIMINARY; PRT; 348 AA.

AC Q9ALV7; 01-JUN-2001 (TREMblrel. 17, Created)
DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)
DT 01-OCT-2002 (TREMblrel. 22, Last annotation update)
DE Acidic repeat protein.

OS Treponema pallidum (subsp. pertenue) (Yaws treponeme).
OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema.
OX NCBI_TaxId=168;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CDC2;
RA Liu H., Steiner B., Rodas B.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF342806; AAK01460.2; -
SQ SEQUENCE 348 AA; 37936 MW; EA446BD82344592 CRC64;

Query Match 100.0%; Score 101; DB 2; Length 348;
Best local similarity 100.0%; Pred. No. 6.2e-07;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVEDVPKVVPEPASEREGGER 20
Db 128 EVEDVPKVVPEPASEREGGER 147

RESULT 2

Q93CA3 PRELIMINARY; PRT; 393 AA.

AC Q93CA3; 01-DEC-2001 (TREMblrel. 19, Created)
DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)
DT 01-OCT-2002 (TREMblrel. 22, Last annotation update)
DE Acidic repeat protein.

OS Treponema pallidum (subsp. pertenue) (Yaws treponeme).
OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema.
OX NCBI_TaxId=168;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CDC1;
RA Liu H., Steiner B.M., Rodas B.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF411126; AAL07373.1; -
SQ SEQUENCE 393 AA; 42852 MW; C2D9198A1BB82B5 CRC64;

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OM protein - protein search, using sw model

Run on: January 28, 2005, 11:12:20 ; Search time 17.5517 Seconds

(without alignments)
655.635 Million cell updates/sec

Title: US-10-017-168-16

Perfect score: 101

Sequence: 1 EVENPKVPEPASEREGGER 20

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: 1: uniprot_sprot; 2: uniprot_tramb1;

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	101	100.0	432	2	051953
2	96	95.0	348	2	09ALV7
3	96	95.0	393	2	093CA3
4	96	95.0	428	2	09ALV6
5	96	95.0	548	2	093CA4
6	92	91.1	256	2	083448
7	78	77.2	227	2	083449
8	51	50.5	1174	2	062043
9	51	50.5	1174	2	BAC98029
10	50	49.5	187	2	09S1J8
11	50	49.5	193	2	0941I5
12	49.5	49.0	357	2	08P8Y8
13	48	47.5	238	2	06ERF9
14	47	46.5	178	2	0700A7
15	47	46.5	178	2	CAG14963
16	47	46.5	256	2	08WV22
17	47	46.5	308	2	098494
18	47	46.5	357	2	06ZAE0
19	47	46.5	357	2	BAD03360
20	47	46.5	383	2	093CV7
21	47	46.5	1699	2	08UXI6
22	46.5	46.0	153	1	Y862_MERTH
23	46	45.5	138	2	09FMV2
24	46	45.5	193	2	08POY1
25	46	45.5	250	2	078A15
26	46	45.5	348	2	08N446
27	46	45.5	435	1	ORCS_MOUSE
28	46	45.5	435	1	BAC39250
29	46	45.5	499	1	MPA2_ARATH
30	46	45.5	554	2	09JHT9
31	46	45.5	556	2	Q7SGY1

ALIGNMENTS

32	46	45.5	620	2	0923H2	Q923H2 mus musculus
33	46	45.5	710	2	08CHT1	Q8CHT1 mus musculus
34	46	45.5	756	2	075B14	Q75B14 ashya gose
35	46	45.5	756	2	AAS51683	AAS51683 ashya go
36	46	45.5	877	1	SYV_MERTH	Q6861 methanobact
37	46	45.5	1310	2	07PDP2	Q7PDP2 plasmodium
38	46	45.5	1350	1	VG72_ICHV1	Q00103 ictaluriid h
39	46	45.5	1697	2	08JUG7	Q8JUG7 normal-k-lik
40	46	45.5	1697	2	08JUL0	Q8JUL0 normal-k-lik
41	46	45.5	2192	2	08IBW7	Q8IBW7 plasmodium
42	45.5	45.0	792	2	08CPY0	Q8CPY0 staphylococ
43	45	44.6	119	2	06P8R8	Q6P8R8 bacillus ch
44	45	44.6	119	2	073FA6	Q73FA6 bacillus ch
45	45	44.6	119	2	081J50	Q81J50 bacillus ce

RESULT 1

ID	051953	PRELIMINARY;	PRT;	432 AA.
AC	051953;			
DT	01-JUN-1998 (TREMBLrel. 06, Created)			
DT	01-JUN-1998 (TREMBLrel. 06, Last sequence update)			
DT	01-OCT-2002 (TREMBLrel. 22, Last annotation update)			
DE	Acidic repeat protein.			
OS	Treponema pallidum.			
OC	Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema.			
OX	NCBI_TaxID=160;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=Nichols;			
RA	Steiner B.M., Rodas B.;			
RL	Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AF015824; AAB94541.1; -			
SO	SEQUENCE 432 AA; 46364 MW; 8PE1E4C55CE846A23 CRC64;			

Query Match 100.0%; Score 101; DB 2; Length 432;
Best Local Similarity 100.0%; Pred. No. 3.9e-07;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	EVENPKVPEPASEREGGER 20
Db	228	EVENPKVPEPASEREGGER 247

RESULT 2

ID	09ALV7	PRELIMINARY;	PRT;	348 AA.
AC	09ALV7;			
DT	01-JUN-2001 (TREMBLrel. 17, Created)			
DT	01-DEC-2001 (TREMBLrel. 19, Last sequence update)			
DT	01-OCT-2002 (TREMBLrel. 22, Last annotation update)			
DE	Acidic repeat protein.			
OS	Name=arp; pallidum (subsp. pertenne) (Yaws treponeme).			
OS	Treponema pallidum (subsp. pertenne) (Yaws treponeme).			
OC	Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema.			
OX	NCBI_TaxID=168;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=CDC2;			
RA	Liu H., Steiner B.;			
RL	Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.			
RN	(2)			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=CDC2;			
RA	Liu H., Steiner B.M., Rodas B.;			
RL	Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AF342806; AAK01460.2; -			
SO	SEQUENCE 348 AA; 37936 MW; EAA446BD82344592 CRC64;			

Query Match 95.0%; Score 96; DB 2; Length 348;

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OM protein - protein search, using sw model

Run on: January 28, 2005, 11:05:24 ; Search time 3.11606 Seconds
(without alignments)
617.555 Million cell updates/sec

Title: US-10-017-168-16

Perfect score: 101

Sequence: 1 EVENVPKXVEPASERREGGER 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-Processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: p1r1: *
2: p1r2: *
3: p1r3: *
4: p1r4: *

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	92	91.1	256	2 F71326
2	78	77.2	227	2 F71326
3	50	49.5	184	2 D84603
4	47	46.5	308	2 T17946
5	46.5	46.0	153	1 B6215
6	46	45.5	897	2 B69202
7	46	45.5	1350	2 G36793
8	45	44.6	220	2 S26885
9	45	44.6	344	2 JCS602
10	45	44.6	344	2 JCS601
11	45	44.6	682	1 S22700
12	44	43.6	178	2 E95994
13	44	43.6	217	2 C37944
14	44	43.6	229	2 B37944
15	44	43.6	229	2 A37944
16	44	43.6	278	2 S36101
17	44	43.6	312	2 E64072
18	44	43.6	341	2 S20827
19	44	43.6	341	2 S26686
20	44	43.6	793	2 S67070
21	43	42.6	99	2 A55819
22	43	42.6	135	2 S56887
23	43	42.6	275	2 F75102
24	43	42.6	289	2 T01257
25	43	42.6	313	2 D86668
26	43	42.6	315	2 D81131
27	43	42.6	356	2 B71023
28	43	42.6	382	2 T08301
29	43	42.6	547	2 E70650

30	43	42.6	554	2 E85015	hypothetical prote
31	43	42.6	559	2 T01724	hypothetical prote
32	43	42.6	566	2 T33926	hypothetical prote
33	43	42.6	1805	2 A34736	neatin - rat
34	42.5	42.1	272	2 B71618	mezoicite surface
35	42	41.6	345	2 A83526	hypothetical prote
36	42	41.6	369	2 A39157	probable RNA helic
37	42	41.6	463	2 T51194	hypothetical prote
38	42	41.6	490	2 E70649	probable regulator
39	42	41.6	623	2 G72412	hypothetical prote
40	42	41.6	688	2 B42161	cGMP-gated cation
41	42	41.6	1143	2 A87488	DNA polymerase III
42	42	41.6	1151	2 T24541	hypothetical prote
43	42	41.6	1272	2 C64513	hypothetical prote
44	42	41.6	1537	2 J04172	DNA (cytosine-5')-
45	41.5	41.1	338	2 S78045	erythrocyte membra

ALIGNMENTS

RESULT 1

F71326

hypothetical protein TP0433 - syphilis spirochete

C:Species: Treponema pallidum subsp. pallidum (syphilis spirochete)

C:Date: 24-Jul-1998 #sequence_revise 24-Jul-1998 #text_change 09-Jul-2004

C:Accession: F71326

R:Fraser, C.M.; Norris, S.J.; Weinstein, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gw

ron, U.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Uettrback, T.; Mc

they, L.; Weidman, J.; Smith, H.O.; Venter, J.C.

Science 281, 375-388, 1998

A:Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.

A:Reference number: A71250; MUID:98332770; PMID:9665876

A:Accession: F71326

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-256 <COL>

A:Cross-references: UNIPROT:O83448; GB:AE001220; GB:AE000520; NID:g3322705; PIDN:AAC65

A:Experimental source: strain Nichols

C:Genetics:

A:Gene: TP0433

Query Match 91.1%; Score 92; DB 2; Length 256;

Best Local Similarity 90.0%; Pred. No. 1.6e-06;

Matches 18; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 EVENVPKXVEPASERREGGER 20

DB 184 EVEDAPKXVEPASERREGGER 203

RESULT 2

G71326

hypothetical protein TP0434 - syphilis spirochete

C:Species: Treponema pallidum subsp. pallidum (syphilis spirochete)

C:Date: 24-Jul-1998 #sequence_revise 24-Jul-1998 #text_change 09-Jul-2004

C:Accession: G71326

R:Fraser, C.M.; Norris, S.J.; Weinstein, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gw

ron, U.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Uettrback, T.; Mc

they, L.; Weidman, J.; Smith, H.O.; Venter, J.C.

Science 281, 375-388, 1998

A:Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.

A:Reference number: A71250; MUID:98332770; PMID:9665876

A:Accession: G71326

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-227 <COL>

A:Cross-references: UNIPROT:O83449; GB:AE001220; GB:AE000520; NID:g3322705; PIDN:AAC65

A:Experimental source: strain Nichols

C:Genetics:

A:Gene: TP0434

Query Match 77.2%; Score 78; DB 2; Length 227;

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OM protein - protein search, using SW model

Run on: January 28, 2005, 10:59:24 ; Search time 18.9507 Seconds
(without alignments)
378.592 Million cell updates/sec

Title: US-10-017-168-17

Perfect score: 101
Sequence: 1 EVEDAPKVPKVPASEREGGER 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: A_Geneseq_23Sep04:*

- 1: Geneseqp1980s:*
- 2: Geneseqp1990s:*
- 3: Geneseqp2000s:*
- 4: Geneseqp2001s:*
- 5: Geneseqp2002s:*
- 6: Geneseqp2003as:*
- 7: Geneseqp2003bs:*
- 8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	101	100.0	20	4	AAB48329 T. pallid
2	101	100.0	432	4	AAB48316 T. pallid
3	97	96.0	20	4	AAB48327 T. pallid
4	97	96.0	232	4	AAB48317 T. pallid
5	97	96.0	312	4	AAB48318 T. pallid
6	92	91.1	20	4	AAB48328 T. pallid
7	91	90.1	20	4	AAB48320 T. pallid
8	78	77.2	20	4	AAB48330 T. pallid
9	77	76.2	20	4	AAB48321 T. pallid
10	65	64.4	21	4	AAB48325 T. pallid
11	64	63.4	19	4	AAB48319 T. pallid
12	53	52.5	26	4	AAB48326 T. pallid
13	48	47.5	296	4	ABG15624 Novel hum
14	47	46.5	79	3	ABG15624 Novel hum
15	47	46.5	187	3	AAAG1629 Arabidops
16	47	46.5	187	3	AAAG1629 Arabidops
17	47	46.5	434	3	AAAG1629 Arabidops
18	47	46.5	434	3	AAAG1629 Arabidops
19	47	46.5	434	3	AAAG1629 Arabidops
20	47	46.5	612	4	ABG15624 Arabidops
21	47	46.5	612	4	ABG15624 Arabidops
22	46	45.5	261	8	ADJ76332 Marker ge
23	46	45.5	437	4	ABM15867 Mycobacte
24	46	45.5	547	6	ABM15867 Mycobacte
25	46	45.5	571	7	ABO77402 Pseudomon

26	46	45.5	1007	4	AAB50660 Aab50660 C. elegan
27	46	45.5	1226	3	AAAG4239 Aag4239 Arabidops
28	46	45.5	1321	3	AAAG4238 Aag4238 Arabidops
29	46	45.5	1351	3	AAAG4237 Aag4237 Arabidops
30	45	44.6	109	4	AAU40366 Aau40366 Propionib
31	45	44.6	109	6	ABM36885 Abm36885 Human pro
32	45	44.6	170	6	ADAS5215 Ada55215 Human pro
33	45	44.6	266	4	AAB80279 Aab80279 Human pro
34	45	44.6	266	4	AAB64379 Aab64379 Human aci
35	45	44.6	266	4	AAM39738 Aam39738 Human pol
36	45	44.6	277	4	AAB80305 Aab80305 Human pro
37	45	44.6	277	4	AAB80347 Aab80347 Human pro
38	45	44.6	288	4	AAAB80343 Aam41524 Human pol
39	45	44.6	289	4	AAAB80343 Aam41524 Human pol
40	45	44.6	304	3	AAAB57037 Aab57037 Human pro
41	45	44.6	510	8	ADQ08680 Adq08680 Clostr. int
42	45	44.6	519	6	ABU20235 Abu20235 Murine BH
43	45	44.6	579	8	AAO24552 Aao24552 Drosophi
44	45	44.6	944	4	ABM60979 Abm60979 Drosophi
45	45	44.6	1841	2	AAW22605 Aaw22605 Ty lactone

ALIGNMENTS

RESULT 1
AAB48329
ID AAB48329 standard; peptide: 20 AA.
XX
AC AAB48329;
XX
DT 20-Apr-2001 (first entry)
XX
DE T. pallidum acidic repeat protein immunogenic peptide arp 11.
XX
KW Treponema pallidum; acidic repeat protein; arp; immunogenic; syphilis;
KW yaws; bejel.
XX
OS Treponema pallidum.
XX
PN W0200077486-A2.
XX
PD 21-DEC-2000.
XX
PE 14-JUN-2000; 2000MO-US016425.
XX
PF 14-JUN-1999; 99US-0138981P.
XX
PR (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PA Liu H, Steiner B, Rhodes B;
PI WPI; 2001-080711/09.
XX
DR
XX
PT Detecting Treponema pallidum in blood, saliva, etc., by detecting
PT formation of a complex between immunogenic peptides of acidic repeat
PT protein of the bacterium and an antibody present in the biological
PT sample.
XX
PS Claim 15; Fig 11; 73pp; English.
XX
XX The invention relates to a method of detecting presence of Treponema
XX pallidum (TP), anti-treponemal antibodies (Abs), or both in a biological
XX sample that involves contacting an acidic repeat protein (arp), or one or
XX more isolated immunogenic TP peptides of arp with an Ab containing
XX biological sample and then detecting the formation of a complex between
XX immunogenic peptides and Ab. The presence of the complex indicates the
XX presence of TP. The method is thus useful for diagnosing syphilis, yaws,
XX and bejel diseases. The immunogenic peptides or the Abs raised against
XX arp, as part of an immunogenic composition, are useful for inducing a
XX protective immune response against syphilis, yaws or bejel caused by TP.
XX Sequences AAB48319-AAB48330 represent immunogenic peptides of T. pallidum
XX arp protein

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OM protein - protein search, using sw model

Run on: January 28, 2005, 11:05:24 ; Search time 3.11606 Seconds
(without alignments)
617.555 Million cell updates/sec

Title: US-10-017-168-17

Perfect score: 101

Sequence: 1 EVEDAPKVEPASEREGGER 20

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	101	100.0	256	2 F71326	hypothetical prote
2	78	77.2	227	2 G71326	hypothetical prote
3	51	50.5	151	2 T24541	hypothetical prote
4	47.5	47.0	153	1 B69215	conserved hypotnet
5	47	46.5	184	2 D84603	hypothetical prote
6	47	46.5	210	2 C87305	hypothetical prote
7	47	46.5	434	2 T47545	monodehydroascorba
8	47	46.5	668	1 QOBEW1	US2 proteain - hum
9	46	45.5	428	2 T32952	hypothetical prote
10	46	45.5	547	2 E70650	phosphoglucosyltrans
11	46	45.5	1408	2 T47671	P-91glycoprotein-11k
12	45	44.6	133	2 T36525	hypothetical prote
13	45	44.6	382	2 T08301	hypothetical prote
14	44.5	44.1	467	2 AH3437	DNA repair protein
15	44	43.6	82	1 QPBO	micro glutamic aci
16	44	43.6	168	1 T22246	response regulator
17	44	43.6	220	2 A75287	hypothetical prote
18	44	43.6	297	2 F70572	hypothetical prote
19	44	43.6	437	2 C35147	integrase homolog
20	44	43.6	1106	1 TVHUGL	transforming prote
21	43	42.6	133	2 T07910	hypothetical prote
22	43	42.6	306	2 T00177	hypothetical prote
23	43	42.6	306	2 G89988	hypothetical prote
24	43	42.6	308	2 T17946	hypothetical prote
25	43	42.6	356	2 B71023	hypothetical prote
26	43	42.6	357	2 H71122	hypothetical prote
27	43	42.6	414	2 A69866	3-oxoacyl-[acyl-ca
28	43	42.6	542	2 E84250	acetyl-CoA synthet
29	43	42.6	852	2 T06310	hypothetical prote

30	43	42.6	1135	2 T30561	Scythe protein - A
31	42.5	42.1	525	2 JN0443	transcription init
32	42.5	42.1	946	2 D96503	protein P9C16.9 (i
33	42.5	42.1	2149	2 T47655	hypothetical prote
34	42	41.6	135	2 S56687	histone H2B153 - w
35	42	41.6	223	2 JX0222	ubiquitin thiolest
36	42	41.6	463	2 T51194	hypothetical prote
37	42	41.6	554	2 JN0094	neurofilament prot
38	42	41.6	733	2 S23468	ococyte-specific pr
39	42	41.6	925	2 G88175	protein T24H7.2 (i
40	42	41.6	1032	2 D83637	serine/threonine p
41	42	41.6	1076	2 S44764	C27D11.1 protein
42	42	41.6	1272	2 C64513	hypothetical prote
43	42	41.6	1350	2 G36793	hypothetical prote
44	41	40.6	73	2 S59954	ribosomal protein
45	41	40.6	99	2 A53819	nonhistone chromos

ALIGNMENTS

RESULT 1

F71326 hypothetical protein TP0433 - syphilis spirochete

C/Species: Treponema pallidum subsp. pallidum (syphilis spirochete)

C/Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 09-Jul-2004

C/Accession: F71326

R/Fraser, C.M.; Norris, S.J.; Weinstein, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gw
rson, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Uterback, T.; Mc
they, L.; Weidman, J.; Smith, H.O.; Venter, J.C.
Science 281, 375-388, 1998

A/Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.
A/Reference number: A71250; MUID:98332770; PMID:9665876

A/Accession: F71326

A/Status: preliminary; nucleic acid sequence not shown; translation not shown

A/Molecule type: DNA

A/Residues: 1-256 <COL>

A/Cross-references: UNIPROT:O83448; GB:AE001220; GB:AE000520; NID:G3322705; PIDN:AAC65

A/Experimental source: strain Nichols

C/Genetics:

A/Gene: TP0433

Query Match 100.0%; Score 101; DB 2; Length 256;
Best Local Similarity 100.0%; Pred. No. 9.2e-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVEDAPKVEPASEREGGER 20

Db 184 EVEDAPKVEPASEREGGER 203

RESULT 2

G71326 hypothetical protein TP0434 - syphilis spirochete

C/Species: Treponema pallidum subsp. pallidum (syphilis spirochete)

C/Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 09-Jul-2004

C/Accession: G71326

R/Fraser, C.M.; Norris, S.J.; Weinstein, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gw
rson, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Uterback, T.; Mc
they, L.; Weidman, J.; Smith, H.O.; Venter, J.C.
Science 281, 375-388, 1998

A/Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.

A/Reference number: A71250; MUID:98332770; PMID:9665876

A/Accession: G71326

A/Status: preliminary; nucleic acid sequence not shown; translation not shown

A/Molecule type: DNA

A/Residues: 1-227 <COL>

A/Cross-references: UNIPROT:O83449; GB:AE001220; GB:AE000520; NID:G3322705; PIDN:AAC65

A/Experimental source: strain Nichols

C/Genetics:

A/Gene: TP0434

Query Match 77.2%; Score 78; DB 2; Length 227;

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OM protein - protein search, using SW model

Run on: January 28, 2005, 11:12:20 ; Search time 17.5517 Seconds
(without alignments)
655.635 Million cell updates/sec

Title: US-10-017-168-17
Perfect score: 101
Sequence: 1 EVEDAPKVEBPASEREGGER 20

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 1825181 segs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: Uniprot 02: *
1: uniprot_sprot: *
2: uniprot_trembl: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	101	100.0	256	2	083448	083448 treponema p
2	101	100.0	432	2	051953	051953 treponema p
3	101	100.0	548	2	093CA4	093CA4 treponema p
4	97	96.0	348	2	09ALV7	09ALV7 treponema p
5	97	96.0	393	2	093CA3	093CA3 treponema p
6	97	96.0	428	2	09ALV6	09ALV6 treponema p
7	78	77.2	227	2	083449	083449 treponema p
8	52	51.5	2192	2	081BW7	081BW7 treponema p
9	51	50.5	1165	2	070KPE	070KPE plasmidum
10	51	50.5	1165	2	070KPE	070KPE caenorhabdi
11	50	49.5	434	2	075UW6	075UW6 brassica ol
12	50	49.5	434	2	093X74	093X74 brassica ra
13	50	49.5	434	2	093X74	093X74 brassica ra
14	50	49.5	572	1	081493	081493 brassica
15	49	48.5	151	2	084S51	084S51 chromobacte
16	49	48.5	151	2	084S51	084S51 oryza sativ
17	49	48.5	294	2	06UGG2	06UGG2 enterobacte
18	49	48.5	294	2	06UGG2	06UGG2 enterobacte
19	48	47.5	769	2	075BK7	075BK7 ashyia goes
20	48	47.5	769	2	075BK7	075BK7 ashyia goes
21	47.5	47.0	2223	2	081D12	081D12 plasmidum
22	47.5	47.0	153	1	1862_METT	1862_METT mus muscu
23	47	46.5	130	2	08CC10	08CC10 mus muscu
24	47	46.5	168	2	08LH12	08LH12 oryza sativ
25	47	46.5	187	2	09S1U8	09S1U8 arabidopsis
26	47	46.5	193	2	0941I5	0941I5 arabidopsis
27	47	46.5	210	2	09AA20	09AA20 caulobacter
28	47	46.5	344	2	098HGO	098HGO rhizobium i
29	47	46.5	357	2	06ZAE0	06ZAE0 oryza sativ
30	47	46.5	357	2	06ZAE0	06ZAE0 oryza sat
31	47	46.5	434	1	MDA3_ARATH	MDA3_ARATH arabidopsis
31	47	46.5	612	2	09VG45	09VG45 drosophila

32	47	46.5	612	2	096019	096019 drosophila
33	47	46.5	668	1	U52_HCMVA	U52_HCMVA human cytom
34	47	46.5	668	2	07M6N1	07M6N1 human cytom
35	47	46.5	668	2	AAA46006	AAA46006 human cyr
36	47	46.5	1174	2	06ZQ43	06ZQ43 mus muscu
37	47	46.5	1174	2	BAC98029	BAC98029 mus muscu
38	47	46.5	1475	2	06CBP1	06CBP1 yarrowia li
39	46	45.5	238	2	06ERP9	06ERP9 oryza sativ
40	46	45.5	261	2	09QUP7	09QUP7 mus muscu
41	46	45.5	262	2	075Z26	075Z26 mus muscu
42	46	45.5	262	2	088346	088346 mus muscu
43	46	45.5	262	2	BAC82459	BAC82459 mus muscu
44	46	45.5	295	2	09S056	09S056 clostridium
45	46	45.5	547	2	P95090	P95090 mycobacteri

ALIGNMENTS

RESULT 1	083448	PRELIMINARY;	PRT;	256 AA.
ID	083448	PRELIMINARY;	PRT;	256 AA.
AC	083448	PRELIMINARY;	PRT;	256 AA.
DT	01-NOV-1998 (TREMBLrel. 08, Created)			
DT	01-NOV-1998 (TREMBLrel. 08, Last sequence update)			
DT	01-JUN-2003 (TREMBLrel. 24, Last annotation update)			
DE	Hypothetical protein TP0433.			
GN	OrderedLocusNames=TP0433;			
OS	Treponema pallidum.			
OC	Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema.			
OX	NCBI_TaxID=160;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=Nichols;			
RX	MEDLINE=98133770; PubMed=9665876;			
RA	Fraser C.M., Norris S.J., Weinstein G.M., White O., Sutton G.G.,			
RA	Dodson R.J., Gwinn M.L., Hickey E.K., Clayton R.A., Ketchum K.A.,			
RA	Sodergren E., Hardham J.M., McLeod M.P., Salzberg S.L., Peterson J.D.,			
RA	Khalak H.G., Richardson D.L., Howell J.K., Chidambaram M.,			
RA	Uterback T.R., McDonald L.A., Artlich P., Bowman C., Cotton M.D.,			
RA	Fuji C., Garland S.A., Hatch B., Horst K., Roberts K.M., Sandusky M.,			
RA	Weldman J.F., Smith H.O., Venter J.C.;			
RT	"Complete genome sequence of Treponema pallidum, the syphilis			
RT	spirochete.";			
RL	Science 281:375-388(1998).			
DR	EMBL; AE001220; AAC65421.1; -			
DR	PIR; F71326; F71326.			
DR	TIGR; TP0433; -			
KX	Complete proteome; Hypothetical protein.			
SQ	SEQUENCE 256 AA; 27453 MW; E90329D25A119E76 CRC64;			
Query Match	100.0%; Score 101; DB 2; Length 256;			
Best Local Similarity	100.0%; Pred. No. 8.1e-07;			
Matches	20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
Qy	1 EVEDAPKVEBPASEREGGER 20			
Db	184 EVEDAPKVEBPASEREGGER 203			
RESULT 2	051953	PRELIMINARY;	PRT;	432 AA.
ID	051953	PRELIMINARY;	PRT;	432 AA.
AC	051953	PRELIMINARY;	PRT;	432 AA.
DT	01-JUN-1998 (TREMBLrel. 06, Created)			
DT	01-JUN-1998 (TREMBLrel. 06, Last sequence update)			
DT	01-OCT-2002 (TREMBLrel. 22, Last annotation update)			
DE	Acidic repeat protein.			
OS	Treponema pallidum.			
OC	Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema.			
OX	NCBI_TaxID=160;			
RN	[1]			
RP	SEQUENCE FROM N.A.			

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OM protein - protein search, using sw model

Run on: January 28, 2005, 10:59:24 ; Search time 18.9507 Seconds
(without alignments)
378.592 Million cell updates/sec

Title: US-10-017-168-18

Perfect score: 106

Sequence: 1 EYEDVPGVGPASGHEGGER 20

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729239 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : A_Geneseq_23sep04.*

1: geneseqp1980s.*
2: geneseqp1980s.*
3: geneseqp2000s.*
4: geneseqp2001s.*
5: geneseqp2002s.*
6: geneseqp2003as.*
7: geneseqp2003bs.*
8: geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	106	100.0	20	4	AAB48330 T. pallid
2	106	100.0	432	4	AAB48316 T. pallid
3	82	77.4	20	4	AAB48327 T. pallid
4	82	77.4	232	4	AAB48317 T. pallid
5	82	77.4	312	4	AAB48318 T. pallid
6	78	73.6	20	4	AAB48329 T. pallid
7	77	72.6	20	4	AAB48328 T. pallid
8	69	65.1	26	4	AAB48326 T. pallid
9	68	64.2	20	4	AAB48320 T. pallid
10	58	54.7	20	4	AAB48321 T. pallid
11	55	51.9	754	7	ADE36201 Klebsell
12	55	51.9	19	4	AAB48316 Klebsell
13	53	50.0	21	4	AAB48319 T. pallid
14	53	50.0	211	6	AAB48325 Propionib
15	52	49.1	211	6	AAB48325 Propionib
16	52	49.1	307	6	ABM64080 Propionib
17	52	49.1	754	7	ABM66113 Propionib
18	52	49.1	754	7	ABM66113 Propionib
19	52	49.1	754	7	ADBS6219 Klebsell
20	52	49.1	754	7	ADBS6219 Klebsell
21	52	49.1	754	7	ADBS6207 Klebsell
22	52	49.1	754	7	ADBS6198 Klebsell
23	52	49.1	754	7	ADBS6222 Klebsell
24	52	49.1	754	7	ADBS6228 Klebsell
25	52	49.1	754	7	ADBS6163 Klebsell
					ADBS6204 Klebsell

26	52	49.1	754	7	ADBS6234 Klebsell
27	52	49.1	754	7	ADBS6216 Klebsell
28	52	49.1	754	7	ADBS6249 Klebsell
29	52	49.1	754	7	ADBS6213 Klebsell
30	52	49.1	754	7	ADBS6237 Klebsell
31	52	49.1	754	7	ADBS6225 Klebsell
32	52	49.1	754	7	ADBS6240 Klebsell
33	52	49.1	754	7	ADBS6226 Klebsell
34	52	49.1	754	7	ADBS6231 Klebsell
35	52	49.1	754	7	ADBS6243 Klebsell
36	51.5	48.6	228	7	ABO84152 Pseudomon
37	50.5	47.6	76	4	ABO60228 Propionib
38	50.5	47.6	76	4	ABM56747 Thermococ
39	50	47.2	340	8	ADNA6982 Protein e
40	50	47.2	350	6	ABU26303 Pseudomon
41	50	47.2	394	7	ABO79086 Pseudomon
42	50	47.2	1504	7	ABO77862 Rat Prote
43	49.5	46.7	683	7	ADDA4887 Streptomy
44	49	46.2	19938	6	ABP76679 Drosophila
45	48.5	45.8	2044	4	ABBE1468 Drosophila

ALIGNMENTS

RESULT 1
AAB48330
ID AAB48330 standard; peptide; 20 AA.

AC AAB48330,
DT 20-APR-2001 (first entry),
XX

DE T. pallidum acidic repeat protein immunogenic peptide a:rp 12.

KM Treponema pallidum, acidic repeat protein; arp, immunogenic; syphilis;
KW yaws; bejel.

XX Treponema pallidum.

OS MO200077486-A2.

XX 21-DEC-2000.

PF 14-JUN-2000; 2000WO-US016425.

PR 14-JUN-1999; 99US-0138981P.

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX Liu H, Steiner B, Rhodes B;

XX WPI, 2001-080711/09.

PT Detecting Treponema pallidum in blood, saliva, etc., by detecting
PT formation of a complex between immunogenic peptides of acidic repeat
PT protein of the bacterium and an antibody present in the biological
PT sample.

XX Claim 15, Fig 11, 73pp, English.

PS The invention relates to a method of detecting presence of Treponema
XX pallidum (TP), anti-treponemal antibodies (Abs), or both in a biological
XX sample that involves contacting an acidic repeat protein (arp), or one or
XX more isolated immunogenic TP peptides of arp with an Ab containing
XX immunogenic peptides and then detecting the formation of a complex between
XX immunogenic peptides and Ab. The presence of the complex indicates the
XX presence of TP. The method is thus useful for diagnosing syphilis, yaws,
XX and bejel diseases. The immunogenic peptides or the Abs raised against
XX arp, as part of an immunogenic composition, are useful for inducing a
XX protective immune response against syphilis, yaws or bejel caused by TP.
XX Sequences AAB48319-AAB48330 represent immunogenic peptides of T. pallidum
XX arp protein

1	106	100.0	227	2	083449	083449 treponema i
2	106	100.0	432	2	051953	051953 treponema i
3	106	100.0	548	2	093CA4	093CA4 treponema i
4	82	77.4	348	2	09ALV7	09ALV7 treponema i
5	82	77.4	393	2	093CA3	093CA3 treponema i
6	82	77.4	428	2	09ALV6	09ALV6 treponema i
7	78	73.6	255	2	083448	083448 treponema i
8	57	53.8	213	2	07UBQ3	07UBQ3 treponema i
9	55	51.9	408	2	08XJL8	08XJL8 synechococcus
10	54	50.9	756	2	075B14	08XJL8 ralsctonia i
11	54	50.9	756	2	AAS51683	075B14 aethya goss
12	53	50.0	370	1	V2R.P1G	AAS51683 aethya g
13	53	50.0	378	1	MSAE.V1BC	P23307 sus scrofa
14	53	50.0	516	2	082NF2	08X1X6 v peptide n
15	51	48.1	370	1	YB1L.FALM1	082NF2 streptomyces
16	51	48.1	350	2	0870P1	P17103 halobacterium
17	50	47.2	188	1	MSA2.RH1ME	0870P1 vibrio parva
18	50	47.2	347	2	07VKX4	0871P1 rhizobium n
19	50	47.2	350	2	09PJ30	07VKX4 helicobacter
20	50	47.2	524	2	08LSK4	09PJ30 campylobact
21	49.5	46.7	683	1	AMBP.RAT	08LSK4 phycomitrite
22	49	46.2	226	2	07UTG3	0888J3 rattus norv
23	49	46.2	358	2	07XZ84	07UTG3 synechococ
24	49	46.2	1165	2	07XZ84	07XZ84 streptomyces
25	49	46.2	1165	2	CAFP1405	07XZ84 casenorbadd
26	48.5	45.8	365	2	08NMJ9	CAFP1485 canothrix
27	48.5	45.8	373	1	08HBM1	08NMJ9 aspergillus
28	48.5	45.8	2044	1	STP.DDOME	08HBM1 cryza betiv
29	48.5	45.8	2052	2	09YRN8	P16520 drosophila
30	48.5	45.8	2051	2	08YRN3	09YRN8 drosophila
31	48.5	45.8	2061	2	AAS65075	08YRN3 drosophila
						AAS65075 drosophila

32	48.5	45.8	2064	1	SIF1 DROME	pe16z1	drosophila
33	48.5	45.8	2022	2	Q9YRN7	Q9YRN7	drosophila
34	48	45.3	260	2	Q985K8	Q985K8	rhizobium
35	48	45.3	325	2	Q9RSY7	Q9RSY7	deinococcus
36	48	45.3	416	2	Q7EL87	Q7EL87	oryzias
37	48	45.3	416	2	BAD00703	BAD00703	oryzias
38	48	45.3	417	2	Q8SVE2	Q8SVE2	bradyrhizob
39	48	45.3	919	2	Q6NZLO	Q6NZLO	mus musculus
40	48	45.3	919	2	AAH6079	AAH6079	mus musculus
41	47.5	44.8	2000	2	Q9Y410	Q9Y410	homo sapiens
42	47	44.3	155	2	Q8ZRZ6	Q8ZRZ6	nitrosomonas
43	47	44.3	160	2	Q8H6T1	Q8H6T1	chlamydomon
44	47	44.3	196	1	MSA2 CAUCA	Q9A9E9	caulobacter
45	47	44.3	227	2	Q8ZQD6	Q8ZQD6	streptomyces

ALIGNMENTS

ID	083449	PRELIMINARY;	PRT;	227 AA.
AC	083449;			
DT	01-NOV-1998 (TREMBLrel. 08, Created)			
DT	01-NOV-1998 (TREMBLrel. 08, Last sequence update)			
DT	01-JUN-2003 (TREMBLrel. 24, Last annotation update)			
DE	Hypothetical protein TP0434.			
OS	OrderedLocustNames=TP0434;			
NC	Treponema pallidum.			
OC	Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema.			
OX	NCBI_TaxID=160;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=Nichols;			
RX	MEDLINE=98333770; PubMed=965876;			
RA	Fraser G.M., Norris S.J., Weinstock G.M., White O., Sutton G.,			
RA	Dodon R.J., Gwinn M.L., Hickey E.K., Clayton R.A., Ketchum K.A.,			
RA	Sodergren E., Hardham J.M., McLeod M.P., Salzberg S.L., Peterson J.D.,			
RA	Khalak H.G., Richardson D.L., Howell J.K., Chidambaram M.,			
RA	Utzberg T.R., McDonald L.A., Artach P., Bowman C., Cotton M.D.,			
RA	Fuji C., Garland S.A., Hatch B., Horst K., Roberts K.M., Sandusky M.,			
RA	Weidman J.F., Smith H.O., Venter J.C.;			
RT	"Complete genome sequence of Treponema pallidum, the syphilis			
RL	spirochete.";			
RL	Science 281:375-388 (1998).			
DR	EMBL; AE001220; AAC65422.1; -.			
DR	PIR; G71326; G71326.			
DR	TIGR; TP0434; -.			
SQ	Complete proteome; Hypothetical protein.			
SEQUENCE	227 AA; 25035 MW; 3FA02711A06E45FE CRC64;			
Query Match	100.0%; Score 106; DB 2; Length 227;			
Best Local Similarity	100.0%; Pred. No. 1.8e-07;			
Matches	20; Conservative 0; Mismatches 0; Indels 0; Gaps			
OY	1 EVEDVPGVVEPAPSGHGGER 20			
DB	47 EVEDVPGVVEPAPSGHGGER 66			
RESULT 2				
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ID	051953	PRELIMINARY;	PRT;	432 AA.
AC	051953;			
DT	01-JUN-1998 (TREMBLrel. 06, Created)			
DT	01-JUN-1998 (TREMBLrel. 06, Last sequence update)			
DT	01-OCT-2002 (TREMBLrel. 22, Last annotation update)			
DE	Acidic repeat protein.			
OS	Treponema pallidum.			
OC	Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema.			
OX	NCBI_TaxID=160;			
RN	[1]			
RP	SEQUENCE FROM N.A.			

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OM nucleic - nucleic search, using bw model

Run on: March 23, 2005, 10:23:13 ; Search time 7357.76 Seconds
(without alignments)
10846.472 Million cell updates/sec

Title: US-10-017-168-19

Perfect score: 1647

Sequence: 1 atgctgtgcgcgcgtgacat.....ttctgaaaagcgcgatga 1647

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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2: gb_hcg:*
3: gb_in:*
4: gb_cm:*
5: gb_ov:*
6: gb_pat:*
7: gb_pl:*
8: gb_pr:*
9: gb_ro:*
10: gb_ro:*
11: gb_ro:*
12: gb_sy:*
13: gb_un:*
14: gb_v1.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1647	100.0	1647	1	AF411124 Treponema
2	1634.4	99.2	2945	6	AX068032 Sequence
3	1634.4	99.2	2946	1	AF015824 Treponema
4	909	55.2	1287	1	AF342807 Treponema
5	858.4	52.1	939	6	AX068036 Sequence
6	823.2	50.0	14268	1	AE001220 Treponema
7	788	47.8	1182	1	AF411126 Treponema
8	653	39.6	1047	1	AF342806 Treponema
9	621.6	37.7	699	6	AX068034 Sequence
10	248.6	15.1	197411	10	AC135961 Mus muscu
11	248.6	14.9	211580	2	AC111089 Mus muscu
12	244.2	14.8	178757	10	AC123509 Mus muscu
13	235	14.3	144093	10	AC108193 Mus muscu
14	234.6	14.2	205054	10	AC098712 Mus muscu
15	233.8	14.2	179206	2	AC124108 Mus muscu
16	233.8	14.2	200574	10	BX005304 Mouse DNA
17	231.8	14.1	124244	10	AL929026 Mouse DNA
18	231.8	14.1	178620	10	AC121865 Mus muscu
19	231	14.0	110000	2	AC120236 Rattus no

20	231	14.0	152618	10	AC127583
21	230.2	14.0	165582	10	AC122020
22	230.2	14.0	194387	10	AC105989
23	230.2	14.0	194736	10	AC126271
24	228.4	13.9	120487	10	AC103637
25	227	13.8	199378	2	AC108256
26	226.8	13.8	171593	10	AC122052
27	226.6	13.8	152435	10	AC121566
28	225.8	13.7	237814	10	AC091464
29	225.4	13.7	187287	10	AL928735
30	223.6	13.6	240931	2	AC107097 Rattus no
31	223.2	13.6	76941	10	BX000698 Mouse DNA
32	223.2	13.6	157754	10	AC132313 Mus muscu
33	221.8	13.5	187126	10	AC113315 Mus muscu
34	221.4	13.4	97839	2	AC141520
35	221.4	13.4	215745	10	AC117585
36	221.4	13.4	234988	2	AC102097 Mus muscu
37	220.6	13.4	195690	10	AC098726 Mus muscu
38	220.2	13.4	157152	10	AC114679 Mus muscu
39	216.4	13.1	169003	10	AC115699 Mus muscu
40	216.2	13.1	178501	10	AC121862 Mus muscu
41	214.8	13.0	260625	2	AC096018
42	214.2	13.0	248718	10	AC117629 Mus muscu
43	213.8	13.0	217353	10	AC149611 Mus muscu
44	212.8	12.9	211947	10	AC107828 Mus muscu
45	212.6	12.9	171570	10	AL807807 Mouse DNA

ALIGNMENTS

RESULT 1
AF411124 1647 bp DNA linear BCT 26-SEP-2001
LOCUS
DEFINITION Treponema pallidum subsp. pallidum strain Nichols acidic repeat
protein (arp) gene, complete cds.

ACCESSION AF411124
VERSION AF411124.1 GI:15778312

KEYWORDS Treponema pallidum subsp. pallidum (syphilis treponeme)

ORGANISM Treponema pallidum subsp. pallidum

REFERENCE 1 (bases 1 to 1647) Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema.

AUTHORS Liu, H., Steiner, B.M. and Rodas, B.

TITLE Molecular characterization of the acidic repeat protein gene (arp)

of Treponema pallidum

Unpublished

JOURNAL 2 (bases 1 to 1647)

REFERENCE Liu, H., Steiner, B.M. and Rodas, B.

AUTHORS Direct Submission

TITLE Submitted (17-AUG-2001) National Center for Infectious Diseases,

JOURNAL Centers for Disease Control and Prevention, 1600 Clifton Rd,

Atlanta, GA 30333, USA

FEATURES

source 1.1647

gene /organism="Treponema pallidum subsp. pallidum"

CDS /mol_type="genomic DNA"

/strain="Nichols"

/sub_species="pallidum"

/db_xref="taxon:161"

1.1647

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1.1647

/gene="arp"

/codon_start=1

/transl_table=11

/product="acidic repeat protein"

/protein_id="FAL07372.1"

/db_xref="GI:15778313"

/translation="MFVRSDFPPTAVRISNLEKNAQAQAVVIGAGIPGLLVSLAP

AAAGAGIGVQAVRVRVTLGVGSGSQTSDGLSLAPRVPAPQORPLSPSP

AGHIVPEYRDTVYFPDPRVSPVSRVEDAPKVEPASAEREGREVEDAPKVEPAS

ERRGGRREVDPVKVEPASERBERREVEDAPKVEPASERBERREVEDPVKVEP

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OM nucleic - nucleic search, using sw model

Run on: March 23, 2005, 10:23:13 ; Search time 929.12 Seconds
(without alignments)
10493.597 Million cell updates/sec

Title: US-10-017-168-19

Perfect score: 1647
Sequence: 1 atgtcttgcgcagcagtcacat.....ttctgaaagcgcatga 1647

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_16Dec04:*

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- 2: Geneseq19908:*
- 3: Geneseq20008:*
- 4: Geneseq20018:*
- 5: Geneseq20018:*
- 6: Geneseq20028:*
- 7: Geneseq20028:*
- 8: Geneseq20038:*
- 9: Geneseq20038:*
- 10: Geneseq20038:*
- 11: Geneseq20038:*
- 12: Geneseq20048:*
- 13: Geneseq20048:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1634.4	99.2	2945	4	AAC84647
2	858.4	52.1	939	4	AAC84649
3	695.8	42.2	9410	2	AAX20603
4	621.6	37.7	699	4	AAC84648
5	206.4	12.5	1926	10	ADK65580
6	206.2	12.5	1926	3	AAAS0254
7	206.2	12.5	1926	4	AAAF82902
8	206.2	12.5	2580	3	AAAF75454
9	206.2	12.5	2580	6	AAAF64275
10	206.2	12.5	5452	2	AAAF90923
11	206.2	12.5	8705	12	AAZ23778
12	206.2	12.5	9480	12	ADP64415
13	206.2	12.5	9600	6	AAV21683
14	206.2	12.5	10285	6	ABST1027
15	206.2	12.5	10285	6	ABST6453
16	206.2	12.5	10330	12	ADL67154
17	206.2	12.5	10380	2	AAZ22248
18	206.2	12.5	10477	12	ADL67152
19	206.2	12.5	10516	12	ADL67150
20	206.2	12.5	10516	12	ADL67150

C	21	206.2	12.5	10561	12	ADL67148	AdL67148 Plasmid P
C	22	206.2	12.5	10596	2	AAQ51731	AaQ51731 Plasmid P
C	23	206.2	12.5	10596	2	AAK15650	AaK15650 Nucleoid
C	24	206.2	12.5	10596	2	AAK10348	AaK10348 Plasmid P
C	25	206.2	12.5	10615	12	ADL67175	AdL67175 Plasmid P
C	26	206.2	12.5	10774	12	ADL67153	AdL67153 Plasmid P
C	27	206.2	12.5	10921	12	ADL67151	AdL67151 Plasmid P
C	28	206.2	12.5	10961	12	ADL67149	AdL67149 Plasmid P
C	29	206.2	12.5	11006	12	ADL67147	AdL67147 Plasmid P
C	30	206.2	12.5	11059	12	ADL67176	AdL67176 Plasmid P
C	31	206.2	12.5	11693	13	ADL12379	AdL12379 Vector PC
C	32	206.2	12.5	11924	12	ADP007395	AdP007395 Modified
C	33	206.2	12.5	12242	12	ADP007394	AdP007394 Modified
C	34	206.2	12.5	16080	3	AAAS9553	AAAS9553 DNA clone
C	35	206.2	12.5	17753	12	ADL71910	AdL71910 Expressio
C	36	206.2	12.5	17281	12	ADN12161	AdN12161 Epsrein-B
C	37	203.6	12.4	12733	6	ABK98631	AbK98631 Vector PE
C	38	203.6	12.4	12733	9	ACD13882	AcD13882 L. lactis
C	39	203.6	12.4	12739	6	ABK98592	AbK98592 Vector PE
C	40	203.6	12.4	12739	9	ACD13843	AcD13843 Plasmid P
C	41	202	12.3	30191	12	ADQ97854	AdQ97854 Mouse can
C	42	199.8	12.1	1925	2	AAK90924	AaK90924 Epsrein B
C	43	191.2	11.6	799	2	AAV5831	AaV5831 Nucleoid
C	44	177.8	10.8	795	2	AAV5830	AaV5830 PlGA Inse
C	45	163.8	9.9	3127	12	ADN12154	AdN12154 Kaposi's s

ALIGNMENTS

RESULT 1	AAAC84647	standard; DNA; 2945 BP.
ID	AAAC84647	
AC	AAAC84647	
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DT	11-SEP-2003	(revised)
DT	20-APR-2001	(first entry)
XX		
DE	T. pallidum acidic repeat protein (arp) encoding DNA.	
XX		
KW	Treponema pallidum; acidic repeat protein; arp; immunogenic; syphilis;	
KW	yaws; bejel; de.	
XX		
OS	Treponema pallidum; ssp. pallidum.	
XX		
FH	Key	Location/Qualifiers
FT	CDS	919..2217
FT		/*tag= a
XX		
XX	WO200077486-A2.	
XX		
XX	21-DEC-2000.	
XX		
PF	14-JUN-2000; 2000WC-US016425.	
XX		
PR	14-JUN-1999; 99US-0138981P.	
XX		
PA	(USSH) US DEPT HEALTH & HUMAN SERVICES.	
XX		
PI	Liu H, Steiner B, Rhodes B;	
XX		
DR	WPI; 2001-080711/09.	
XX	P-PSDB; AAB48316.	
XX		
PT	Detecting Treponema pallidum in blood, saliva, etc., by detecting	
PT	formation of a complex between immunogenic peptides of acidic repeat	
PT	protein of the bacterium and an antibody present in the biological	
PT	sample.	
XX		
XX	Claim 19; Fig 5; 73pp; English.	
XX	The invention relates to a method of detecting presence of Treponema	